



# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES

<130> D0072.NP

<140> US 10,029,345

<141> 2001-12-20

<150> US 60,256,868

<151> 2000-12-20

<150> US 60,280,186

<151> 2001-03-30

<150> US 60,387,735

<151> 2001-05-01

<150> US 60,195,848

<151> 2001-04-05

<150> US 60,300,465

<151> 2001-05-25

<160> 203

<170> PatentIn version 3.0

<210> 1

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<212> DNA

<213> HOMO SAPIENS

<400> 1

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catgcagggc ttggtcgaac aggt 144

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<211> 48

<212> PFT

<213> HOMO SAPIENS

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Leu Val Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser  
1 5 10 15

Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln  
20 25 30

Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly

35

40

45

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33

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 gttctgttg gacctggggc tgcggcacct ggtgtccctg acggagcgcg ggcacctca 180  
 cagcgacagc tgccccggcc tcacctgca ccgcctgcgc atccccgact tctgcccgcc 240  
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 cctggtgaag gagcggggct tggctgcagg agatgcaatt gctgaaatcc gacgactacg 420  
 acccgggccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480  
 gaaataaggg gccttagtac ccttctacca ggcctcact cccttcccc atgttgtcga 540  
 tggggccaga gatgaaggga agtggactaa agtattaaac cctctagctc ccattggctg 600  
 aagacactga agtagccac cctgcaggc aggtcctgat tgaaggggag gcttgtactg 660  
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<214> HOMO SAPIENS

<220>

<221> VARIANT

<222> (162)..(162)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (200)..(200)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (203)..(203)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (214)..(214)

<223> wherein 'Xaa' is any amino acid.

<220>

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<222> (224)..(224)

<223> wherein 'Xaa' is any amino acid.

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Pro	Asn	Phe	Ser	Trp	Val	Leu	Pro	Gly	Arg	Leu	Ala	Gly	Leu	Ala	Leu
			20					25					30		
Pro	Arg	Leu	Pro	Ala	His	Tyr	Gln	Phe	Leu	Leu	Asp	Leu	Gly	Val	Arg
		35					40					45			
His	Leu	Val	Ser	Leu	Thr	Glu	Arg	Gly	Pro	Pro	His	Ser	Asp	Ser	Cys
	50					55					60				
Pro	Gly	Leu	Thr	Leu	His	Arg	Leu	Arg	Ile	Pro	Asp	Phe	Cys	Pro	Pro
65					70					75					80
Ala	Pro	Asp	Gln	Ile	Asp	Arg	Phe	Val	Gln	Ile	Val	Asp	Glu	Ala	Asn
			85						90					95	
Ala	Arg	Gly	Glu	Ala	Val	Gly	Val	His	Cys	Ala	Leu	Gly	Phe	Gly	Arg
		100						105					110		
Thr	Gly	Thr	Met	Leu	Ala	Cys	Tyr	Leu	Val	Lys	Glu	Arg	Gly	Leu	Ala
		115					120					125			

Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Pro Ile  
130 135 140

Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr  
145 150 155 160

Lys Xaa Gly Ala Leu Val Pro Phe Tyr Gln Ala Leu Thr Pro Leu Pro  
165 170 175

His Val Val Asp Gly Ala Arg Asp Glu Gly Lys Trp Thr Lys Val Leu  
180 185 190

Asn Pro Leu Ala Pro Ile Gly Xaa Arg His Xaa Ser Ser Pro Pro Leu  
195 200 205

Gln Ala Gly Pro Asp Xaa Arg Gly Gly Leu Tyr Cys Phe Val Glu Xaa  
210 215 220

Met Ser Phe Thr Asn Gln Gly Lys Lys Lys Lys Lys Lys Arg Lys Lys  
225 230 235 240

Lys Lys Lys Lys Lys Lys Lys Arg  
245

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ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180  
ggaagcatcc aggttcgga ctggcctttt gatgatggta cagcaccatc cagccagata 240  
attgataact ggttaaaact tatgaaaaat aaatttcattg aagatcctgg ttgttgatt 300  
gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgcc tagctttaat 360  
tgaagggtgga atgaaatatg aaaatgtagt acagttcatc agataaaagt gacatggaac 420  
ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgcacct 480  
cagaaatccc agaaataact gtttccttca g 511

<10> 8  
<11> 170  
<12> PFT  
<13> HOMO SAPIENS

<120>  
<121> Variant



<322> (49)..(49)  
 <323> wherein 'Xaa' is any amino acid.

<327>  
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 <329> (156)..(156)  
 <330> wherein 'Xaa' is any amino acid.

<336>  
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 <338> (142)..(142)  
 <339> wherein 'Xaa' is any amino acid.

<340>  
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 <342> (110)..(110)  
 <343> wherein 'Xaa' is any amino acid.

<350>  
 <351> Variant  
 <352> (121)..(121)  
 <353> wherein 'Xaa' is any amino acid.

<360>  
 <361> Variant  
 <362> (127)..(127)  
 <363> wherein 'Xaa' is any amino acid.

<370>  
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 <372> (155)..(155)  
 <373> wherein 'Xaa' is any amino acid.

<400> 8

Met	Ala	Arg	Met	Asn	Leu	Pro	Ala	Ser	Val	Asp	Ile	Ala	Tyr	Lys	Asn
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Val	Arg	Phe	Leu	Ile	Thr	His	Asn	Pro	Thr	Asn	Thr	Tyr	Phe	Asn	Arg
			20					25					30		

Phe	Leu	Gln	Glu	Leu	Lys	Gln	Asp	Gly	Val	Thr	Thr	Ile	Val	Arg	Val
		35					40					45			

Xaa	Lys	Ala	Thr	Tyr	Asn	Ile	Ala	Leu	Leu	Glu	Lys	Gly	Ser	Ile	Gln
	50					55					60				

Val	Pro	Asp	Trp	Pro	Phe	Asp	Asp	Gly	Thr	Ala	Pro	Ser	Ser	Gln	Ile
65					70					75				80	

Ile Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro  
                   85                                  90                                  95  
 Gly Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Xaa Ala Pro  
                   100                                  105                                  110  
 Val Ala Ser Cys Pro Ser Phe Asn Xaa Arg Trp Asn Glu Ile Xaa Lys  
                   115                                  120                                  125  
 Cys Ser Thr Val His Gln Ile Lys Val Thr Trp Asn Phe Xaa Gln Gln  
                   130                                  135                                  140  
 Thr Thr Phe Val Phe Gly Glu Ile Leu Ser Xaa Asn Met Leu Ala Pro  
                   145                                  150                                  155                                  160  
 Gln Lys Ser Gln Lys Xaa Leu Phe Pro Ser  
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 accaccaaga actgttaacc acatgtgcta cctatgacc actccagggt caggctgacc 150  
 cagctggagg gagagcctca ttctgactac atcaatgcca acttggtccc aggtacacc 200  
 cgccacagg agttcattgc ctctcagggg cctctcaaga aaacactgga gaacttctgg 250  
 cggctgggtgc gggagcagca ggtcgcacc atcatcatgc cgaccatcag catggagaac 300  
 gggaggggtgc tgtgtgagca ttactggctg accgactcta cccgggacac ccatggtcac 350  
 atcaccatcc acctcctagc tgaggagcct gaggatgagt ggaccaagcg ggaattccag 400  
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 tcgaccaca gcatacctga ggctccagc tccctgctcg cctttatgga gctggtagag 500  
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tectatgacc gttctaggg gcagttttct ccggtggagg agagccccc tgacgacatg 1080  
 cctctctgga agccaatgat ctgtctctctg baggggtggc cctctgggcy tgatcatacg 1140  
 gtgttgactg gccccgcagg gccaaaggag ctctggggagc tgggtgtggca gcacagggct 1200  
 catgtgcttg tctctctttg ccacccaat gtcctggaga aggaattctg gccaacggag 1260  
 atgagcccg tagtcacaga catgggtgagc gtgcactggg tggctgagag cagcacagca 1320  
 ggctgggttct gtacccctct caggggtcaca catgggggaga gcaggaagga aaggaggggtg 1380  
 cagagactgc aatttcata cctggagcct gggcatgagc tgcccgccac caccctgctg 1440  
 ccttctctgg ctgctgtggg ccagtgtctc tctcggggca acaacaagaa gccgggcaca 1500  
 ctgtcagcc actccaaaca ggggtcaacc cagctgggca ccttctctgg catggagcag 1560  
 ctgtcagc aggcagggctc tgagtgcacc gtggatatct ttaacgtggc cctgcagcag 1620  
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<220>  
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<220>  
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 <222> (180)..(180)  
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<220>  
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 <222> (201)..(201)  
 <223> wherein 'Xaa' is any amino acid.

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Phe Leu Lys Phe Glu Glu Leu Lys Glu Val Ser Lys Glu Gln Pro Arg  
 20 25 30

Leu	Glu	Ala	Glu	Tyr	Pro	Ala	Asn	Thr	Thr	Lys	Asn	Cys	Xaa	Pro	His	35	40	45
Val	Leu	Pro	Tyr	Asp	His	Ser	Arg	Val	Arg	Leu	Thr	Gln	Leu	Glu	Gly	50	55	60
Glu	Pro	His	Ser	Asp	Tyr	Ile	Asn	Ala	Asn	Leu	Val	Pro	Gly	Tyr	Thr	65	70	75
Arg	Pro	Gln	Glu	Phe	Ile	Ala	Ser	Gln	Gly	Pro	Leu	Lys	Lys	Thr	Leu	85	90	95
Glu	Asn	Phe	Trp	Arg	Leu	Val	Arg	Glu	Gln	Gln	Val	Arg	Ile	Ile	Ile	100	105	110
Met	Pro	Thr	Ile	Ser	Met	Glu	Asn	Gly	Arg	Val	Leu	Cys	Glu	His	Tyr	115	120	125
Trp	Leu	Thr	Asp	Ser	Thr	Pro	Asp	Thr	His	Gly	His	Ile	Thr	Ile	His	130	135	140
Leu	Leu	Ala	Glu	Glu	Pro	Glu	Asp	Glu	Trp	Thr	Lys	Arg	Glu	Phe	Gln	145	150	155
Leu	Gln	His	Val	Val	Gln	Gln	His	Gln	Arg	Arg	Val	Glu	Gln	Leu	Gln	165	170	175
Phe	Thr	Thr	Xaa	Ser	Asp	His	Ser	Ile	Leu	Glu	Ala	Pro	Ser	Ser	Leu	180	185	190
Leu	Ala	Phe	Met	Glu	Leu	Val	Gln	Xaa	Gln	Ala	Arg	Ala	Thr	Gln	Gly	195	200	205
Val	Gly	Pro	Ile	Leu	Val	His	Cys	Arg	Gly	Cys	Pro	Cys	Gly	Val	Gly	210	215	220
Met	Gly	Arg	Thr	Gly	Thr	Phe	Val	Ala	Leu	Ser	Arg	Leu	Leu	Gln	Gln	225	230	235
Leu	Glu	Glu	Glu	Gln	Met	Val	Asp	Val	Phe	His	Ala	Val	Tyr	Ala	Leu	245	250	255
Arg	Met	His	Gln	Pro	Leu	Met	Ile	Gln	Thr	Leu	Ser	Gln	Tyr	Val	Phe	260	265	270
Leu	His	Ser	Cys	Leu	Leu	Asn	Lys	Ile	Leu	Glu	Gly	Pro	Phe	Asn	Ile	275	280	285
Ser	Glu	Ser	Trp	Pro	Ile	Ser	Val	Thr	Asp	Leu	Pro	Gln	Ala	Cys	Ala	290	295	300
Lys	Arg	Ala	Ala	Ser	Ala	Asn	Ala	Gly	Phe	Leu	Lys	Glu	Tyr	Glu	Ala	305	310	315
Ile	Lys	Asp	Glu	Ala	Gly	Phe	Ser	Ala	Pro	Pro	Pro	Gly	Tyr	Glu	Gln	325	330	335

Asp Ser Pro Val Ser Tyr Asp Arg Ser Gln Gly Gln Phe Ser Pro Val  
 340 345 350  
 Glu Glu Ser Pro Pro Asp Asp Met Pro Leu Trp Lys Pro Met Ile Cys  
 355 360 365  
 Ala Leu Gln Gly Gly Pro Ser Gly Arg Asp His Thr Val Leu Thr Gly  
 370 375 380  
 Pro Ala Gly Pro Lys Glu Leu Trp Glu Leu Val Trp Gln His Arg Ala  
 385 390 395 400  
 His Val Leu Val Ser Leu Cys Pro Pro Asn Val Met Glu Lys Glu Phe  
 405 410 415  
 Trp Pro Thr Glu Met Gln Pro Val Val Thr Asp Met Val Thr Val His  
 420 425 430  
 Trp Val Ala Glu Ser Ser Thr Ala Gly Trp Phe Cys Thr Leu Leu Arg  
 435 440 445  
 Val Thr His Gly Glu Ser Arg Lys Glu Arg Glu Val Gln Arg Leu Gln  
 450 455 460  
 Phe Pro Tyr Leu Glu Pro Gly His Glu Leu Pro Ala Thr Thr Leu Leu  
 465 470 475 480  
 Pro Phe Leu Ala Ala Val Gly Gln Cys Cys Ser Arg Gly Asn Asn Lys  
 485 490 495  
 Lys Pro Gly Thr Leu Leu Ser His Ser Asn Lys Gly Ala Thr Gln Leu  
 500 505 510  
 Gly Thr Phe Leu Ala Met Glu Gln Leu Leu Gln Gln Ala Gly Ser Glu  
 515 520 525  
 Cys Thr Val Asp Ile Phe Asn Val Ala Leu Gln Gln Ser Gln Ala Cys  
 530 535 540  
 Gly Leu Met Thr Pro Thr Leu Lys Gln Tyr Val Tyr Leu Tyr Asn Cys  
 545 550 555 560  
 Leu Asn Ser Ala Leu Ala Asp Gly Leu Pro  
 565 570

<210> 11

<211> 63

<212> DNA

<213> HOMO SAPIENS

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60

gag

63

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 aacaagaatt gttaaccaca tgtgctaccc t 91

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 atgccaactt ggcccc 77

<210> 14  
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 aactcttgjc ggctgggtgcg ggagcagcag gtccgcatca tcatcatgcc gaccatcagc 120  
 atggagaang ggagg 135

<210> 15  
 <211> 123  
 <212> DNA  
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 atccaccttc tagctgagga gcttgaggat gagtggacca agcgggaatt ccagctgcag 120  
 cac 123

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aggagcaacc agggcggtggg acccatcctg gtgcactgca g 151

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 gatgcaccag cccctcatga tccagaccct g 151

<210> 18  
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 atctctga 68

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 caatgctggc ttcttgaagg agtacgag 88

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 gtctcct 67

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<210> 22  
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 ggtgactggc cccgcagggc caaaggagct ctgggagctg gtgtggcagc acagggctca 120  
 tgtgcttctc tctcttggcc cacccaatgt catggagaag 150

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 cgggagcaaca acaagaagcc gggcacactg ctacgccact ccaa 164

<210> 25  
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 <212> DNA  
 <213> HOMO SAPIENS

<400> 25  
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 gcttgagctc accgtggata tctttaacgt ggccctgcag cagtctcagg cctgtggcct 120  
 tatgaccaca acactg 136

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 <211> 57  
 <212> RNA  
 <213> HOMO SAPIENS

<400> 26



57

400 27

13

Asp Thr Ile Gly Lys Glu Lys Leu Phe His Phe Thr Glu Glu Thr Pro  
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 275 280 285  
 Ser Asp Tyr Glu Thr Thr Ser Gln Pro Tyr Trp Trp Asp Ser Ala Ser  
 290 295 300  
 Ala Ala Pro Glu Ser Glu Asp Glu Phe Val Ser Val Leu Pro Met Glu  
 305 310 315 320  
 Tyr Glu Asn Asn Ser Thr Leu Ser Glu Thr Glu Lys Ser Thr Ser Gly  
 325 330 335  
 Ser Phe Ser Phe Phe Pro Val Gln Met Ile Leu Thr Trp Leu Pro Pro  
 340 345 350  
 Lys Pro Pro Thr Ala Phe Asp Gly Phe His Ile His Ile Glu Arg Glu  
 355 360 365  
 Glu Asn Phe Thr Glu Tyr Leu Met Val Asp Glu Glu Ala His Glu Phe  
 370 375 380  
 Val Ala Glu Leu Lys Glu Pro Gly Lys Tyr Lys Leu Ser Val Thr Thr  
 385 390 395 400  
 Phe Ser Ser Ser Gly Ser Cys Glu Thr Arg Lys Ser Gln Ser Ala Lys  
 405 410 415  
 Ser Leu Ser Phe Tyr Ile Ser Pro Ser Gly Glu Trp Ile Glu Glu Leu  
 420 425 430  
 Thr Glu Lys Pro Gln His Val Ser Val His Val Leu Ser Ser Thr Thr  
 435 440 445  
 Ala Leu Met Ser Trp Thr Ser Ser Gln Glu Asn Tyr Asn Ser Thr Ile  
 450 455 460  
 Val Ser Val Val Ser Leu Thr Cys Gln Lys Gln Lys Glu Ser Gln Arg  
 465 470 475 480  
 Leu Glu Lys Gln Tyr Cys Thr Gln Val Asn Ser Ser Lys Pro Ile Ile  
 485 490 495  
 Glu Asn Leu Val Pro Gly Ala Gln Tyr Gln Val Val Ile Tyr Leu Arg  
 500 505 510  
 Lys Gly Pro Leu Ile Gly Pro Pro Ser Asp Pro Val Thr Phe Ala Ile  
 515 520 525  
 Val Pro Thr Gly Ile Lys Asp Leu Met Leu Tyr Pro Leu Gly Pro Thr  
 530 535 540  
 Ala Val Val Leu Ser Trp Thr Arg Pro Tyr Leu Gly Val Phe Arg Lys  
 545 550 555 560

Tyr	Val	Val	Glu	Met	Phe	Tyr	Phe	Asn	Pro	Ala	Thr	Met	Thr	Ser	Glu	
				555					570					575		
Trp	Thr	Thr	Tyr	Tyr	Glu	Ile	Ala	Ala	Thr	Val	Ser	Leu	Thr	Ala	Ser	
			580					585					590			
Val	Arg	Ile	Ala	Asn	Leu	Leu	Pro	Ala	Trp	Tyr	Tyr	Asn	Phe	Arg	Val	
		595					600					605				
Thr	Met	Val	Thr	Trp	Gly	Asp	Pro	Glu	Leu	Ser	Cys	Cys	Asp	Ser	Ser	
	610					615					620					
Thr	Ile	Ser	Phe	Ile	Thr	Ala	Pro	Val	Ala	Pro	Glu	Ile	Thr	Ser	Val	
	625				630					635					640	
Glu	Tyr	Phe	Asn	Ser	Leu	Leu	Tyr	Ile	Ser	Trp	Thr	Tyr	Gly	Asp	Asp	
			645						650					655		
Thr	Thr	Asp	Leu	Ser	His	Ser	Arg	Met	Leu	His	Trp	Met	Val	Val	Ala	
		660						665					670			
Glu	Gly	Lys	Lys	Lys	Ile	Lys	Lys	Ser	Val	Thr	Arg	Asn	Val	Met	Thr	
		675					680					685				
Ala	Ile	Leu	Ser	Leu	Pro	Pro	Gly	Asp	Ile	Tyr	Asn	Leu	Ser	Val	Thr	
	690					695					700					
Ala	Cys	Thr	Glu	Arg	Gly	Ser	Asn	Thr	Ser	Met	Leu	Arg	Leu	Val	Lys	
	705				710					715					720	
Leu	Glu	Pro	Ala	Pro	Pro	Lys	Ser	Leu	Phe	Ala	Val	Asn	Lys	Thr	Gln	
			725						730					735		
Thr	Ser	Val	Thr	Leu	Leu	Trp	Val	Glu	Glu	Gly	Val	Ala	Asp	Phe	Phe	
		740						745					750			
Glu	Val	Phe	Cys	Gln	Gln	Val	Gly	Ser	Ser	Gln	Lys	Thr	Lys	Leu	Gln	
	755						760					765				
Glu	Pro	Val	Ala	Val	Ser	Ser	His	Val	Val	Thr	Ile	Ser	Ser	Leu	Leu	
	770					775					780					
Pro	Ala	Thr	Ala	Tyr	Asn	Cys	Ser	Val	Thr	Ser	Phe	Ser	His	Asp	Ser	
	785				790					795					800	
Pro	Ser	Val	Pro	Thr	Phe	Ile	Ala	Val	Ser	Thr	Met	Val	Thr	Glu	Met	
			805						810					815		
Asn	Pro	Asn	Val	Val	Val	Ile	Ser	Val	Leu	Ala	Ile	Leu	Ser	Thr	Leu	
			820						825				830			
Leu	Ile	Gly	Leu	Leu	Leu	Val	Thr	Leu	Ile	Ile	Leu	Arg	Lys	Lys	His	
	835						840					845				
Leu	Gln	Met	Ala	Arg	Glu	Cys	Gly	Ala	Gly	Thr	Phe	Val	Asn	Phe	Ala	
	850					855					860					

Ser Leu Glu Arg Asp Gly Lys Leu Pro Tyr Asn Trp Ser Lys Asn Gly  
 865 870 875 880  
 Leu Lys Lys Arg Lys Leu Thr Asn Pro Val Gln Leu Asp Asp Phe Asp  
 885 890 895  
 Ala Tyr Ile Lys Asp Met Ala Lys Asp Ser Asp Tyr Lys Phe Ser Leu  
 900 905 910  
 Gln Phe Glu Glu Leu Lys Leu Ile Gly Leu Asp Ile Pro His Phe Ala  
 915 920 925  
 Ala Asp Leu Pro Leu Asn Arg Cys Lys Asn Arg Tyr Thr Asn Ile Leu  
 930 935 940  
 Pro Tyr Asp Phe Ser Arg Val Arg Leu Val Ser Met Asn Glu Glu Glu  
 945 950 955 960  
 Gly Ala Asp Tyr Ile Asn Ala Asn Tyr Ile Pro Gly Tyr Asn Ser Pro  
 965 970 975  
 Gln Glu Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Arg Asn Asp  
 980 985 990  
 Phe Trp Lys Met Val Leu Gln Gln Lys Ser Gln Ile Ile Val Met Leu  
 995 1000 1005  
 Thr Gln Cys Asn Glu Lys Arg Arg Val Lys Cys Asp His Tyr Trp  
 1010 1015 1020  
 Pro Phe Thr Glu Glu Pro Ile Ala Tyr Gly Asp Ile Thr Val Glu  
 1025 1030 1035  
 Met Ile Ser Glu Glu Glu Gln Asp Asp Trp Ala Cys Arg His Phe  
 1040 1045 1050  
 Arg Ile Asn Tyr Ala Asp Glu Met Gln Asp Val Met His Phe Asn  
 1055 1060 1065  
 Tyr Thr Ala Trp Pro Asp His Gly Val Pro Thr Ala Asn Ala Ala  
 1070 1075 1080  
 Glu Ser Ile Leu Gln Phe Val His Met Val Arg Gln Gln Ala Thr  
 1085 1090 1095  
 Lys Ser Lys Gly Pro Met Ile Ile His Cys Ser Ala Gly Val Gly  
 1100 1105 1110  
 Arg Thr Gly Thr Phe Ile Ala Leu Asp Arg Leu Leu Gln His Ile  
 1115 1120 1125  
 Arg Asp His Glu Phe Val Asp Ile Leu Gly Leu Val Ser Glu Met  
 1130 1135 1140  
 Arg Ser Tyr Arg Met Ser Met Val Gln Thr Glu Glu Gln Tyr Ile  
 1145 1150 1155

Phe Ile His Gln Cys Val Gln Leu Met Trp Met Lys Lys Lys Gln  
 1160 1165 1170

Gln Phe Cys Ile Ser Asp Val Ile Tyr Glu Asn Val Ser Lys Ser  
 1175 1180 1185

<010> 28  
 <011> 405  
 <012> PRT  
 <013> Mus musculus

<400> 28

Met Val Thr Glu Val Asn Pro Asn Val Val Val Ile Ser Val Leu Ala  
 1 5 10 15

Ile Leu Ser Thr Leu Leu Ile Gly Leu Leu Leu Val Thr Leu Val Ile  
 20 25 30

Leu Arg Lys Lys His Leu Gln Met Ala Arg Glu Cys Gly Ala Gly Thr  
 35 40 45

Phe Val Asn Phe Ala Ser Leu Glu Arg Glu Gly Lys Leu Pro Tyr Ser  
 50 55 60

Trp Arg Arg Ser Val Phe Ala Leu Leu Thr Leu Leu Pro Ser Cys Leu  
 65 70 75 80

Trp Thr Asp Tyr Leu Leu Ala Phe Tyr Ile Asn Pro Trp Ser Lys Asn  
 85 90 95

Gly Leu Lys Lys Arg Lys Leu Thr Asn Pro Val Glu Leu Asp Asp Phe  
 100 105 110

Asp Ser Tyr Ile Lys Asp Met Ala Lys Asp Ser Asp Tyr Lys Phe Ser  
 115 120 125

Leu Gln Phe Glu Glu Leu Lys Leu Ile Gly Leu Asp Ile Pro His Phe  
 130 135 140

Ala Ala Asp Leu Pro Leu Asn Arg Cys Lys Asn Arg Tyr Thr Asn Ile  
 145 150 155 160

Leu Pro Tyr Asp Phe Ser Arg Val Arg Leu Val Ser Met Asn Glu Glu  
 165 170 175

Glu Gly Ala Asp Tyr Ile Asn Ala Asn Tyr Ile Pro Gly Tyr Asn Ser  
 180 185 190

Pro Gln Glu Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Arg Asn  
 195 200 205

Asp Phe Trp Lys Met Val Leu Gln Gln Lys Ser His Ile Ile Val Met  
 210 215 220

Leu Thr Gln Cys Asn Glu Lys Arg Arg Val Lys Cys Asp His Tyr Trp

225	230	235	240
Pro Phe Thr Glu Glu	Pro Ile Ala Tyr Gly	Asp Ile Thr Val Glu Met	
245	250	255	
Val Ser Glu Glu Glu Glu	Asp Trp Ala Ser Arg His Phe Arg Ile		
260	265	270	
Asn Tyr Ala Asp Glu Ala Gln	Asp Val Met His Phe Asn Tyr Thr Gly		
275	280	285	
Trp Pro Asp His Gly Val	Pro Pro Ala Asn Ala Ala Glu Ser Ile Leu		
290	295	300	
Gln Phe Val Phe Thr Val Arg Gln Gln Ala Ala Lys Ser Lys Gly Pro			
305	310	315	320
Met Ile Ile His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile			
325	330	335	
Ala Leu Asp Arg Leu Leu Gln His Ile Arg Asp His Glu Phe Val Asp			
340	345	350	
Ile Leu Gly Leu Val Ser Glu Met Arg Ser Tyr Arg Met Ser Met Val			
355	360	365	
Gln Thr Glu Glu Gln Tyr Ile Phe Ile His Gln Cys Val Gln Leu Met			
370	375	380	
Trp Leu Arg Lys Lys Gln Gln Phe Cys Ile Ser Asp Val Ile Tyr Glu			
385	390	395	400
Asn Val Ser Lys Ser			
405			

<210> 29  
 <211> 303  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 29

Met Ser Phe Lys Glu Val Ser Thr Glu Asn Gly Val Leu Thr Pro Leu	
1	15
Ile Thr Ile Lys Glu Lys Ala Tyr Met Ile Ile Glu Gly Leu Asn Glu	
20	30
Glu Glu Ile Glu Leu Leu Asn Thr Arg Leu Pro Lys Leu Ser Lys Lys	
35	45
Ala Leu Ala Arg Asn Arg Tyr Ser Asn Ile Val Pro Tyr Glu Asn Thr	
50	60
Arg Val Arg Leu Asp Pro Met Trp Lys Glu Ala Cys Asp Tyr Ile Asn	
65	80

Ala Ser Ile Val Lys Ile Pro Ser Gly Lys Thr Phe Ile Ala Thr Gln  
 85 90 95  
 Gly Pro Thr Ser Asn Ser Ile Asp Val Phe Trp Lys Met Val Trp Gln  
 100 105 110  
 Ser Val Pro Lys Ser Gly Ile Ile Val Met Leu Thr Lys Leu Arg Glu  
 115 120 125  
 Arg His Arg Leu Lys Cys Asp Ile Tyr Trp Pro Val Glu Leu Phe Glu  
 130 135 140  
 Thr Leu Asn Ile Gly Asp Leu Ser Val Ile Leu Val Lys Val Tyr Thr  
 145 150 155 160  
 Leu Thr Ser Leu Asn Glu Val Gln Val Arg Glu Phe Glu Leu Asn Lys  
 165 170 175  
 Asp Gly Val Lys Lys Lys Ile Leu His Phe Tyr Tyr Asn Gly Trp Pro  
 180 185 190  
 Asp Phe Gly Ala Pro His Thr Phe Ser Leu Leu Ser Leu Thr Arg Tyr  
 195 200 205  
 Ile Lys Ser Leu Ser Tyr Ser Pro Asp Phe Glu Thr Ala Pro Ile Ile  
 210 215 220  
 Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Thr Phe Met Ala Leu  
 225 230 235 240  
 Phe Glu Ile Leu Ser Gln Thr Asp Asp Ser Thr Ser Thr Ser Lys Phe  
 245 250 255  
 Glu Val Asp Asn Ile Ala Asn Ile Val Ser Ser Leu Arg Ser Gln Arg  
 260 265 270  
 Met Gln Ser Val Gln Ser Val Asp Gln Leu Val Phe Leu Tyr Thr Val  
 275 280 285  
 Ser Gln Glu Leu Leu Gln Gly Lys Glu Phe Leu Leu Pro Gln Leu  
 290 295 300

<210> 30  
 <211> 580  
 <212> PFT  
 <213> homo sapiens

<400> 30

Met Lys Asp Arg Leu Tyr Phe Ala Thr Leu Arg Asn Arg Pro Lys Ser  
 1 5 10 15  
 Thr Val Asn Thr His Tyr Phe Ser Ile Asp Glu Glu Leu Val Tyr Glu  
 20 25 30  
 Asn Phe Tyr Ala Asp Phe Gly Pro Leu Asn Leu Ala Met Val Tyr Arg  
 35 40 45

Tyr	Cys	Cys	Lys	Leu	Asn	Lys	Lys	Leu	Lys	Ser	Tyr	Ser	Leu	Ser	Arg	
50						55					60					
Lys	Lys	Ile	Val	His	Tyr	Thr	Cys	Phe	Asp	Gln	Arg	Lys	Arg	Ala	Asn	
65					70					75					80	
Ala	Ala	Phe	Leu	Ile	Gly	Ala	Tyr	Ala	Val	Ile	Tyr	Leu	Lys	Lys	Thr	
				85					90					95		
Pro	Glu	Glu	Ala	Tyr	Arg	Ala	Leu	Leu	Ser	Gly	Ser	Asn	Pro	Pro	Tyr	
			100					105					110			
Leu	Pro	Phe	Arg	Asp	Ala	Ser	Phe	Gly	Asn	Cys	Thr	Tyr	Asn	Leu	Thr	
		115					120					125				
Ile	Leu	Asp	Cys	Leu	Gln	Gly	Ile	Arg	Lys	Gly	Leu	Gln	His	Gly	Phe	
130						135					140					
Phe	Asp	Phe	Glu	Thr	Ile	Asp	Val	Asp	Glu	Tyr	Glu	His	Tyr	Glu	Arg	
145					150					155					160	
Val	Glu	Asn	Gly	Asp	Phe	Asn	Cys	Ile	Val	Pro	Gly	Lys	Phe	Leu	Ala	
				165					170					175		
Phe	Ser	Gly	Pro	His	Pro	Lys	Ser	Lys	Ile	Glu	Asn	Gly	Tyr	Pro	Leu	
			180					185					190			
His	Ala	Pro	Glu	Ala	Tyr	Phe	Pro	Tyr	Phe	Lys	Lys	His	Asn	Val	Thr	
		195					200					205				
Ala	Val	Val	Arg	Leu	Asn	Lys	Lys	Ile	Tyr	Glu	Ala	Lys	Arg	Phe	Thr	
210						215					220					
Asp	Ala	Gly	Phe	Glu	His	Tyr	Asp	Leu	Phe	Phe	Ile	Asp	Gly	Ser	Thr	
225					230					235					240	
Pro	Ser	Asp	Asn	Ile	Val	Arg	Arg	Phe	Leu	Asn	Ile	Cys	Glu	Asn	Thr	
			245						250					255		
Glu	Gly	Ala	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	Arg	Thr	Gly	
			260					265					270			
Thr	Leu	Ile	Ala	Cys	Tyr	Val	Met	Lys	His	Tyr	Arg	Phe	Thr	His	Ala	
		275					280					285				
Glu	Ile	Ile	Ala	Trp	Ile	Arg	Ile	Cys	Arg	Pro	Gly	Ser	Ile	Ile	Gly	
290					295						300					
Pro	Gln	Gln	His	Phe	Leu	Glu	Glu	Lys	Gln	Ala	Ser	Leu	Trp	Val	Gln	
305					310					315					320	
Gly	Asp	Ile	Phe	Arg	Ser	Lys	Leu	Lys	Asn	Arg	Pro	Ser	Ser	Glu	Gly	
			325						330					335		
Ser	Ile	Asn	Lys	Ile	Leu	Ser	Gly	Leu	Asp	Asp	Met	Ser	Ile	Gly	Gly	
		340						345					350			



Asn Leu Ser Lys Thr Gln Asn Met Glu Arg Phe Gly Glu Asp Asn Leu  
355 360 365

Glu Asp Asp Asp Val Glu Met Lys Asn Gly Ile Thr Gln Gly Asp Lys  
370 375 380

Leu Arg Ala Leu Lys Ser Gln Arg Gln Pro Arg Thr Ser Pro Ser Cys  
385 390 395 400

Ala Phe Arg Ser Asp Asp Thr Lys Gly His Pro Arg Ala Val Ser Gln  
405 410 415

Pro Phe Arg Leu Ser Ser Ser Leu Gln Gly Ser Ala Val Thr Leu Lys  
420 425 430

Thr Ser Lys Met Ala Leu Ser Pro Ser Ala Thr Ala Lys Arg Ile Asn  
435 440 445

Arg Thr Ser Leu Ser Ser Gly Ala Thr Val Arg Ser Phe Ser Ile Asn  
450 455 460

Ser Arg Leu Ala Ser Ser Leu Gly Asn Leu Asn Ala Ala Thr Asp Asp  
465 470 475 480

Pro Glu Asn Lys Lys Thr Ser Ser Ser Ser Lys Ala Gly Phe Thr Ala  
485 490 495

Ser Pro Phe Thr Asn Leu Leu Asn Gly Ser Ser Gln Pro Thr Thr Arg  
500 505 510

Asn Tyr Pro Glu Leu Asn Asn Asn Gln Tyr Asn Arg Ser Ser Asn Ser  
515 520 525

Asn Gly Gly Asn Leu Asn Ser Pro Pro Gly Pro His Ser Ala Lys Thr  
530 535 540

Glu Glu His Thr Thr Ile Leu Arg Pro Ser Tyr Thr Gly Leu Ser Ser  
545 550 555 560

Ser Ser Ala Arg Phe Leu Ser Arg Ser Ile Pro Ser Leu Gln Ser Glu  
565 570 575

Tyr Val His Tyr  
580

<210> 31  
<211> 459  
<212> PRT  
<213> homo sapiens

<400> 31

Met Lys Arg Lys Ser Glu Arg Arg Ser Ser Trp Ala Ala Ala Pro Pro  
1 5 10 15

Cys Ser Arg Arg Cys Ser Ser Thr Ser Pro Gly Val Lys Lys Ile Arg

20					25					30					
Ser	Ser	Thr	Gln	Gln	Asp	Pro	Arg	Arg	Arg	Asp	Pro	Gln	Asp	Asp	Val
		35					40					45			
Tyr	Leu	Asp	Ile	Thr	Asp	Arg	Leu	Cys	Phe	Ala	Ile	Leu	Tyr	Ser	Arg
	50					55					60				
Pro	Lys	Ser	Ala	Ser	Asn	Val	His	Tyr	Phe	Ser	Ile	Asp	Asn	Glu	Leu
65					70					75				80	
Glu	Tyr	Glu	Asn	Phe	Tyr	Ala	Asp	Phe	Gly	Pro	Leu	Asn	Leu	Ala	Met
			85						90					95	
Val	Tyr	Arg	Tyr	Cys	Cys	Lys	Ile	Asn	Lys	Lys	Leu	Lys	Ser	Ile	Thr
			100					105					110		
Met	Leu	Arg	Lys	Lys	Ile	Val	His	Phe	Thr	Gly	Ser	Asp	Gln	Arg	Lys
	115						120					125			
Gln	Ala	Asn	Ala	Ala	Phe	Leu	Val	Gly	Cys	Tyr	Met	Val	Ile	Tyr	Leu
	130					135					140				
Gly	Arg	Thr	Pro	Glu	Glu	Ala	Tyr	Arg	Ile	Leu	Ile	Phe	Gly	Glu	Thr
145					150					155				160	
Ser	Tyr	Ile	Pro	Phe	Arg	Asp	Ala	Ala	Tyr	Gly	Ser	Cys	Asn	Phe	Tyr
				165						170				175	
Ile	Thr	Leu	Leu	Asp	Cys	Phe	His	Ala	Val	Lys	Lys	Ala	Met	Gln	Tyr
		180						185					190		
Gly	Phe	Leu	Asn	Phe	Asn	Ser	Phe	Asn	Leu	Asp	Glu	Tyr	Glu	His	Tyr
		195					200					205			
Glu	Lys	Ala	Glu	Asn	Gly	Asp	Leu	Asn	Trp	Ile	Ile	Pro	Asp	Arg	Phe
	210					215					220				
Ile	Ala	Phe	Cys	Gly	Pro	His	Ser	Arg	Ala	Arg	Leu	Glu	Ser	Gly	Tyr
225					230					235				240	
His	Gln	His	Ser	Pro	Glu	Thr	Tyr	Ile	Gln	Tyr	Phe	Lys	Asn	His	Asn
				245					250					255	
Val	Thr	Thr	Ile	Ile	Arg	Leu	Asn	Lys	Arg	Met	Tyr	Asp	Ala	Lys	Arg
			260					265					270		
Phe	Thr	Asp	Ala	Gly	Phe	Asp	His	His	Asp	Leu	Phe	Phe	Ala	Asp	Gly
		275					280					285			
Ser	Thr	Pro	Thr	Asp	Ala	Ile	Val	Lys	Glu	Phe	Leu	Asp	Ile	Cys	Glu
	290					295					300				
Asn	Ala	Glu	Gly	Ala	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	Arg
305					310					315				320	
Thr	Gly	Thr	Leu	Ile	Ala	Cys	Tyr	Ile	Met	Lys	His	Tyr	Arg	Met	Thr

325	330	335
Ala Ala Glu Thr Ile Ala Trp Val Arg Ile Cys Arg Pro Gly Ser Val 340	345	350
Ile Gly Pro Gln Gln Gln Phe Leu Val Met Lys Gln Thr Asn Leu Trp 355	360	365
Leu Glu Gly Asp Tyr Phe Arg Gln Lys Leu Lys Gly Gln Glu Asn Gly 370	375	380
Gln His Arg Ala Ala Phe Ser Lys Leu Leu Ser Gly Val Asp Asp Ile 385	390	395
Ser Ile Asn Gly Val Glu Asn Gln Asp Gln Gln Glu Pro Glu Pro Tyr 405	410	415
Ser Asp Asp Asp Glu Ile Asn Gly Val Thr Gln Gly Asp Arg Leu Arg 420	425	430
Ala Leu Lys Ser Arg Arg Gln Ser Lys Thr Asn Ala Ile Pro Leu Thr 435	440	445
Leu Ser Ile Ser Arg Thr Lys Thr Val Leu Arg 450	455	
<210> 32		
<211> 551		
<212> PFT		
<213> Saccharomyces cerevisiae		
<400> 32		
Met Arg Arg Ser Val Tyr Leu Asp Asn Thr Ile Glu Phe Leu Arg Gly 1	5	10
Arg Val Tyr Leu Gly Ala Tyr Asp Tyr Thr Pro Glu Asp Thr Asp Glu 20	25	30
Leu Val Phe Phe Thr Val Glu Asp Ala Ile Phe Tyr Asn Ser Phe His 35	40	45
Leu Asp Phe Gly Pro Met Asn Ile Gly His Leu Tyr Arg Phe Ala Val 50	55	60
Ile Phe His Glu Ile Leu Asn Asp Pro Glu Asn Ala Asn Lys Ala Val 65	70	75
Val Phe Tyr Ser Ser Ala Ser Thr Arg Gln Arg Ala Asn Ala Ala Cys 85	90	95
Met Leu Cys Cys Tyr Met Ile Leu Val Gln Ala Trp Thr Pro His Gln 100	105	110
Val Leu Gln Pro Leu Ala Gln Val Asp Pro Pro Phe Met Pro Phe Arg 115	120	125

Asp	Ala	Gly	Tyr	Ser	Asn	Ala	Asp	Phe	Glu	Ile	Thr	Ile	Gln	Asp	Val	130	135	140
Val	Tyr	Gly	Val	Trp	Arg	Ala	Lys	Glu	Lys	Gly	Leu	Ile	Asp	Leu	His	145	150	155
Ser	Phe	Asn	Leu	Glu	Ser	Tyr	Glu	Lys	Tyr	Glu	His	Val	Glu	Phe	Gly	165	170	175
Asp	Phe	Asn	Val	Leu	Thr	Pro	Asp	Phe	Ile	Ala	Phe	Ala	Ser	Pro	Gln	180	185	190
Glu	Asp	His	Pro	Lys	Gly	Tyr	Leu	Ala	Thr	Lys	Ser	Ser	His	Leu	Asn	195	200	205
Gln	Pro	Phe	Lys	Ser	Val	Leu	Asn	Phe	Phe	Ala	Asn	Asn	Asn	Val	Gln	210	215	220
Leu	Val	Val	Arg	Leu	Asn	Ser	His	Leu	Tyr	Asn	Lys	Lys	His	Phe	Glu	225	230	235
Asp	Ile	Gly	Ile	Gln	His	Leu	Asp	Leu	Ile	Phe	Glu	Asp	Gly	Thr	Cys	245	250	255
Pro	Asp	Leu	Ser	Ile	Val	Lys	Asn	Phe	Val	Gly	Ala	Ala	Glu	Thr	Ile	260	265	270
Ile	Lys	Arg	Gly	Gly	Lys	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	275	280	285
Arg	Thr	Gly	Cys	Leu	Ile	Gly	Ala	His	Leu	Ile	Tyr	Thr	Tyr	Gly	Phe	290	295	300
Thr	Ala	Asn	Glu	Cys	Ile	Gly	Phe	Leu	Arg	Phe	Ile	Arg	Pro	Gly	Met	305	310	315
Val	Val	Gly	Pro	Gln	Gln	His	Trp	Leu	Tyr	Leu	His	Gln	Asn	Asp	Phe	325	330	335
Arg	Glu	Trp	Lys	Tyr	Thr	Thr	Arg	Ile	Ser	Leu	Lys	Pro	Ser	Glu	Ala	340	345	350
Ile	Gly	Gly	Leu	Tyr	Pro	Leu	Ile	Ser	Leu	Glu	Glu	Tyr	Arg	Leu	Gln	355	360	365
Lys	Lys	Lys	Leu	Lys	Asp	Asp	Lys	Arg	Val	Ala	Gln	Asn	Asn	Ile	Glu	370	375	380
Gly	Glu	Leu	Arg	Asp	Leu	Thr	Met	Thr	Pro	Pro	Ser	Asn	Gly	His	Gly	385	390	395
Ala	Leu	Ser	Ala	Arg	Asn	Ser	Ser	Gln	Pro	Ser	Thr	Ala	Asn	Asn	Gly	405	410	415
Ser	Asn	Ser	Phe	Lys	Ser	Ser	Ala	Val	Pro	Gln	Thr	Ser	Pro	Gly	Gln	420	425	430

Pro Arg Lys Gly Gln Asn Gly Ser Asn Thr Ile Glu Asp Ile Asn Asn  
 435 440 445

Asn Arg Asn Pro Thr Ser His Ala Asn Arg Lys Val Val Ile Glu Ser  
 450 455 460

Asn Asn Ser Asp Asp Glu Ser Met Gln Asp Thr Asn Gly Thr Ser Asn  
 465 470 475 480

His Tyr Pro Lys Val Ser Arg Lys Lys Asn Asp Ile Ser Ser Ala Ser  
 485 490 495

Ser Ser Arg Met Glu Asp Asn Glu Pro Ser Ala Thr Asn Ile Asn Asn  
 500 505 510

Ala Ala Asp Asp Thr Ile Leu Arg Gln Leu Leu Pro Lys Asn Arg Arg  
 515 520 525

Val Thr Ser Gly Arg Arg Thr Thr Ser Ala Ala Gly Gly Ile Arg Lys  
 530 535 540

Ile Ser Gly Ser Ile Lys Lys  
 545 550

<210> 33

<211> 173

<212> PRT

<213> homo sapiens

<400> 33

Met Ala Arg Met Asn Arg Pro Ala Pro Val Glu Val Thr Tyr Lys Asn  
 1 5 10 15

Met Arg Phe Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys  
 20 25 30

Phe Ile Glu Glu Leu Lys Lys Tyr Gly Val Thr Thr Ile Val Arg Val  
 35 40 45

Cys Glu Ala Thr Tyr Asp Thr Thr Leu Val Glu Lys Glu Gly Ile His  
 50 55 60

Val Leu Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Ser Asn Gln Ile  
 65 70 75 80

Val Asp Asp Trp Leu Ser Leu Val Lys Ile Lys Phe Arg Glu Glu Pro  
 85 90 95

Gly Cys Cys Ile Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro  
 100 105 110

Val Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asp  
 115 120 125

Ala Val Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys  
 130 135 140

Gln Leu Leu Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe  
 145 150 155 160

Lys Asp Ser Asn Gly His Arg Asn Asn Cys Cys Ile Gln  
 165 170

<E10> 34  
 <E11> 167  
 <E12> PRT  
 <E13> homo sapiens

<400> 34

Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe  
 1 5 10 15

Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu  
 20 25 30

Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala  
 35 40 45

Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp  
 50 55 60

Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp  
 65 70 75 80

Trp Leu Asn Leu Leu Lys Thr Lys Phe Arg Glu Glu Pro Gly Cys Cys  
 85 90 95

Val Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro Val Leu Val  
 100 105 110

Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln  
 115 120 125

Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu  
 130 135 140

Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr  
 145 150 155 160

Asn Gly His Cys Cys Val Gln  
 165

<E10> 35  
 <E11> 167  
 <E12> PRT  
 <E13> Mus musculus

<400> 35

Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe  
 1 5 10 15

Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu  
 20 25 30  
 Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala  
 35 40 45  
 Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp  
 50 55 60  
 Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp  
 65 70 75 80  
 Trp Leu Asn Leu Leu Lys Thr Leu Phe Arg Glu Glu Pro Gly Cys Cys  
 85 90 95  
 Val Ala Val His Cys Val Ala Gly Ile Gly Arg Ala Pro Val Leu Val  
 100 105 110  
 Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln  
 115 120 125  
 Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu  
 130 135 140  
 Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr  
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 Asn Gly His Cys Cys Val Gln  
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 <212> PRT  
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<400> 36

Met Ser Ile Thr Met Arg Gln Lys Asp Leu Arg Pro Ala Pro Ala Leu  
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 Ile Glu Tyr Lys Gly Met Lys Phe Leu Ile Thr Asp Arg Pro Ser Asp  
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 Ile Thr Ile Asn His Tyr Ile Met Glu Leu Lys Lys Asn Asn Val Asn  
 35 40 45  
 Thr Val Val Arg Val Cys Glu Pro Ser Tyr Asn Thr Asp Glu Leu Glu  
 50 55 60  
 Thr Gln Gly Ile Thr Val Lys Asp Leu Ala Phe Glu Asp Gly Thr Phe  
 65 70 75 80  
 Pro Pro Gln Gln Val Val Asp Glu Trp Phe Glu Phe Phe Val Val Leu  
 85 90 95  
 Tyr Arg Tyr Gln Gln Asn Pro Glu Ala Cys Val Ala Val His Cys Val  
 100 105 110

Ala Gly Leu Gly Arg Ala Pro Val Leu Val Ala Leu Ala Leu Ile Glu  
115 120 125

Leu Gly Leu Lys Tyr Glu Ala Ala Val Glu Met Ile Arg Asp Lys Arg  
130 135 140

Arg Gly Ala Ile Asn Ala Lys Gln Leu Ser Phe Leu Glu Lys Tyr Lys  
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Pro Lys Ala Arg Leu Lys His Lys Asn Gly His Lys Asn Ser Cys Ser  
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Val Gln

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<211> 1705  
<212> PRT  
<213> Mus musculus

<400> 37

Met Arg Pro Leu Ile Leu Leu Ala Ala Leu Leu Trp Leu Gln Asp Ser  
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Leu Ala Gln Glu Asp Val Cys Ser Ser Leu Asp Gly Ser Pro Asp Arg  
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Gln Gly Gly Gly Pro Pro Leu Ser Val Asn Val Ser Ser Arg Gly Lys  
35 40 45

Pro Thr Ser Leu Phe Leu Ser Trp Val Ala Ala Glu Pro Gly Gly Phe  
50 55 60

Asp Tyr Ala Leu Cys Leu Arg Ala Met Asn Leu Ser Gly Phe Pro Glu  
65 70 75 80

Gly Gln Gln Leu Gln Ala His Thr Asn Glu Ser Ser Phe Glu Phe His  
85 90 95

Gly Leu Val Pro Gly Ser Arg Tyr Gln Leu Glu Leu Thr Val Leu Arg  
100 105 110

Pro Cys Trp Gln Asn Val Thr Ile Thr Leu Thr Ala Arg Thr Ala Pro  
115 120 125

Thr Val Val Arg Gly Leu Gln Leu His Ser Thr Gly Ser Pro Ala Ser  
130 135 140

Leu Glu Ala Ser Trp Ser Asp Ala Ser Gly Asp Gln Asp Ser Tyr Gln  
145 150 155 160

Leu Leu Leu Tyr His Pro Glu Ser His Thr Leu Ala Cys Asn Val Ser  
165 170 175

Val Ser Pro Asp Thr Leu Ser Tyr Asn Phe Gly Asp Leu Leu Pro Gly



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Ser	Gln	Tyr	Val	Leu	Glu	Val	Ile	Thr	Trp	Ala	Gly	Ser	Leu	His	Ala
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Lys	Thr	Ser	Ile	Leu	Gln	Trp	Thr	Glu	Pro	Val	Pro	Pro	Asp	His	Leu
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Thr	Leu	Arg	Ala	Leu	Gly	Thr	Ser	Ser	Leu	Gln	Ala	Phe	Trp	Asn	Ser
225					230					235					
Ser	Glu	Gly	Ala	Thr	Trp	Phe	His	Leu	Ile	Leu	Thr	Asp	Leu	Leu	Glu
245					250					255					
Gly	Thr	Asn	Leu	Thr	Lys	Val	Val	Arg	Gln	Gly	Ile	Ser	Thr	His	Thr
260					265					270					
Phe	Leu	Arg	Leu	Ser	Pro	Gly	Thr	Pro	Tyr	Gln	Leu	Lys	Ile	Lys	Ala
275					280					285					
Ala	Ala	Gly	Pro	His	Gln	Ile	Trp	Gly	Pro	Asn	Ala	Thr	Glu	Trp	Thr
290					295					300					
Tyr	Pro	Ser	Tyr	Pro	Ser	Asp	Leu	Val	Leu	Thr	Pro	Leu	Trp	Asn	Glu
305					310					315					
Leu	Trp	Ala	Ser	Trp	Lys	Ala	Gly	Gln	Gly	Ala	Arg	Asp	Gly	Tyr	Val
325					330					335					
Leu	Lys	Leu	Ser	Gly	Pro	Val	Glu	Asn	Thr	Thr	Thr	Leu	Gly	Pro	Glu
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Glu	Cys	Asn	Ala	Val	Phe	Pro	Gly	Pro	Leu	Pro	Pro	Gly	His	Tyr	Thr
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Leu	Gly	Leu	Arg	Val	Leu	Ala	Gly	Pro	Tyr	Asp	Ala	Trp	Val	Glu	Gly
370					375					380					
Ser	Ile	Trp	Leu	Ala	Glu	Ser	Ala	Ala	Arg	Pro	Met	Glu	Val	Pro	Gly
385					390					395					
Ala	Arg	Leu	Trp	Leu	Glu	Gly	Leu	Glu	Ala	Thr	Lys	Gln	Pro	Gly	Arg
405					410					415					
Arg	Ala	Leu	Leu	Tyr	Ser	Val	Asp	Ala	Pro	Gly	Leu	Leu	Gly	Asn	Ile
420					425					430					
Ser	Val	Ser	Ser	Gly	Ala	Thr	His	Val	Thr	Phe	Cys	Gly	Leu	Val	Pro
435					440					445					
Gly	Ala	His	Tyr	Arg	Val	Asp	Ile	Ala	Ser	Ser	Met	Gly	Asp	Ile	Thr
450					455					460					
Gln	Ser	Leu	Thr	Gly	Tyr	Thr	Ser	Pro	Leu	Pro	Pro	Gln	Ser	Leu	Glu
465					470					475					
Ile	Ile	Ser	Arg	Asn	Ser	Pro	Ser	Asp	Leu	Thr	Ile	Gly	Trp	Ala	Pro

485																490																495															
Ala	Pro	Gly	Gln	Met	Glu	Gly	Tyr	Lys	Val	Thr	Trp	His	Gln	Asp	Gly																																
500																505																510															
Ser	Gln	Arg	Ser	Pro	Gly	Asp	Leu	Val	Asp	Leu	Gly	Pro	Asp	Ile	Ser																																
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Ser	Leu	Thr	Leu	Lys	Ser	Leu	Val	Pro	Gly	Ser	Cys	Tyr	Thr	Val	Ser																																
530																535																540															
Ala	Trp	Ala	Trp	Ser	Gly	Asn	Leu	Ser	Ser	Asp	Ser	Gln	Lys	Ile	His																																
545																550																555															
Ser	Cys	Thr	Arg	Pro	Ala	Pro	Pro	Thr	Asn	Leu	Ser	Leu	Gly	Phe	Ala																																
565																570																575															
His	Gln	Pro	Ala	Thr	Leu	Arg	Ala	Ser	Trp	Cys	His	Pro	Pro	Gly	Gly																																
580																585																590															
Arg	Asp	Ala	Phe	Gln	Leu	Arg	Leu	Tyr	Arg	Leu	Arg	Pro	Leu	Thr	Leu																																
595																600																605															
Glu	Ser	Glu	Lys	Ile	Leu	Ser	Gln	Glu	Ala	Gln	Asn	Phe	Ser	Trp	Ala																																
610																615																620															
Gln	Leu	Pro	Ala	Gly	Tyr	Glu	Phe	Gln	Val	Gln	Leu	Ser	Thr	Leu	Trp																																
625																630																635															
Gly	Ser	Glu	Glu	Ser	Gly	Ser	Ala	Asn	Thr	Thr	Gly	Trp	Thr	Pro	Pro																																
645																650																655															
Ser	Ala	Pro	Thr	Leu	Val	Asn	Val	Thr	Ser	Glu	Ala	Pro	Thr	Gln	Leu																																
660																665																670															
His	Val	Ser	Trp	Val	His	Ala	Ala	Gly	Asp	Arg	Ser	Ser	Tyr	Gln	Val																																
675																680																685															
Thr	Leu	Tyr	Gln	Glu	Ser	Thr	Arg	Thr	Ala	Thr	Ser	Ile	Val	Gly	Pro																																
690																695																700															
Lys	Ala	Asp	Ser	Thr	Ser	Phe	Trp	Gly	Leu	Thr	Pro	Gly	Thr	Lys	Tyr																																
705																710																715															
Lys	Val	Glu	Ala	Ile	Ser	Trp	Ala	Gly	Pro	Leu	Tyr	Thr	Ala	Ala	Ala																																
725																730																735															
Asn	Val	Ser	Ala	Trp	Thr	Tyr	Pro	Leu	Thr	Pro	Asn	Glu	Leu	Leu	Ala																																
740																745																750															
Ser	Met	Gln	Ala	Gly	Ser	Ala	Val	Val	Asn	Leu	Ala	Trp	Pro	Ser	Gly																																
755																760																765															
Pro	Leu	Gly	Gln	Gly	Thr	Cys	His	Ala	Gln	Leu	Ser	Asp	Ala	Gly	His																																
770																775																780															
Leu	Ser	Trp	Glu	Gln	Pro	Leu	Ser	Leu	Gly	Gln	Asp	Leu	Leu	Met	Leu																																

785		790		795		800
Arg Asn Leu Ile Pro Gly His Thr Val Ser Leu Ser Val Lys Cys Arg	805		810		815	
Ala Gly Pro Leu Gln Ala Ser Thr His Pro Leu Val Leu Ser Val Glu	820		825		830	
Pro Gly Pro Val Glu Asp Val Phe Cys Gln Pro Glu Ala Thr Tyr Leu	835		840		845	
Ser Leu Asn Trp Thr Met Pro Thr Gly Asp Val Ala Val Cys Leu Val	850		855		860	
Glu Val Glu Gln Leu Val Pro Gly Gly Ser Ala His Phe Val Phe Gln	865		870		875	880
Val Asn Thr Ser Glu Asp Ala Leu Leu Leu Pro Asn Leu Thr Pro Thr	885		890		895	
Thr Ser Tyr Arg Leu Ser Leu Thr Val Leu Gly Gly Asn Arg Gln Trp	900		905		910	
Ser Arg Ala Val Thr Leu Val Cys Thr Thr Ser Ala Glu Val Trp His	915		920		925	
Pro Pro Glu Leu Ala Glu Ala Pro Gln Val Glu Leu Gly Thr Gly Met	930		935		940	
Gly Val Thr Val Thr Arg Gly Met Phe Gly Lys Asp Asp Gly Gln Ile	945		950		955	960
Gln Trp Tyr Gly Ile Ile Ala Thr Ile Asn Met Thr Leu Ala Gln Pro	965		970		975	
Ser Gln Glu Ala Ile Asn His Thr Trp Tyr Asp His Tyr Tyr Arg Gly	980		985		990	
His Asp Ser Tyr Leu Ala Leu Leu Phe Pro Asn Pro Phe Tyr Pro Glu	995		1000		1005	
Pro Trp Ala Val Pro Arg Ser Trp Thr Val Pro Val Gly Thr Glu	1010		1015		1020	
Asp Cys Asp Asn Thr Gln Glu Ile Cys Asn Gly His Leu Lys Pro	1025		1030		1035	
Gly Phe Gln Tyr Arg Phe Ser Ile Ala Ala Phe Ser Arg Leu Ser	1040		1045		1050	
Ser Pro Glu Thr Ile Leu Ala Phe Ser Ala Phe Ser Glu Pro Gln	1055		1060		1065	
Ala Ser Ile Ser Leu Val Ala Met Pro Leu Thr Val Met Met Gly	1070		1075		1080	
Thr Val Val Gly Cys Ile Ile Ile Val Cys Ala Val Leu Cys Leu						

1085		1090		1095
Leu Cys Arg Arg Arg Leu	Lys Gly Pro Arg Ser	Glu Lys Asn Gly		
1100	1105	1110		
Phe Ser Gln Glu Leu Met	Pro Tyr Asn Leu Trp	Arg Thr His Arg		
1115	1120	1125		
Pro Ile Pro Ser His Ser	Phe Arg Gln Ser Tyr	Glu Ala Lys Ser		
1130	1135	1140		
Ala Arg Ala His Gln Ala	Phe Phe Gln Glu Phe	Glu Glu Leu Lys		
1145	1150	1155		
Glu Val Gly Lys Asp Gln	Pro Arg Leu Glu Ala	Glu His Pro Ala		
1160	1165	1170		
Asn Ile Thr Lys Asn Arg	Tyr Pro His Val Leu	Pro Tyr Asp His		
1175	1180	1185		
Ser Arg Val Arg Leu Thr	Gln Leu Ser Gly Glu	Pro His Ser Asp		
1190	1195	1200		
Tyr Ile Asn Ala Asn Phe	Ile Pro Gly Tyr Ser	His Pro Gln Glu		
1205	1210	1215		
Ile Ile Ala Thr Gln Gly	Pro Leu Lys Lys Thr	Val Glu Asp Phe		
1220	1225	1230		
Trp Arg Leu Val Trp Glu	Gln Gln Val His Val	Ile Ile Met Leu		
1235	1240	1245		
Thr Val Gly Met Glu Asn	Gly Arg Val Leu Cys	Glu His Tyr Trp		
1250	1255	1260		
Pro Val Asn Ser Thr Pro	Val Thr His Gly His	Ile Thr Thr His		
1265	1270	1275		
Leu Leu Ala Glu Glu Ser	Glu Asp Glu Trp Thr	Arg Arg Glu Phe		
1280	1285	1290		
Gln Leu Gln His Gly Ala	Glu Gln Lys Gln Arg	Arg Val Lys Gln		
1295	1300	1305		
Leu Gln Phe Thr Thr Trp	Pro Asp His Ser Val	Pro Glu Ala Pro		
1310	1315	1320		
Ser Ser Leu Leu Ala Phe	Val Glu Leu Val Gln	Glu Glu Val Lys		
1325	1330	1335		
Ala Thr Gln Gly Lys Gly	Pro Ile Leu Val His	Cys Ser Ala Gly		
1340	1345	1350		
Val Gly Arg Thr Gly Thr	Phe Val Ala Leu Leu	Pro Ala Val Arg		
1355	1360	1365		
Gln Leu Glu Glu Glu Gln	Val Val Asp Val Phe	Asn Thr Val Tyr		

1370		1375		1380
Ile Leu Arg Leu His Arg Pro Leu Met Ile Gln Thr Leu Ser Gln				
1385		1390		1395
Tyr Ile Phe Leu His Ser Cys Leu Leu Asn Lys Ile Leu Glu Gly				
1400		1405		1410
Pro Ser Asp Ala Ser Asp Ser Gly Pro Ile Pro Val Met Asn Phe				
1415		1420		1425
Ala Gln Ala Cys Ala Lys Arg Ala Ala Asn Ala Asn Ala Gly Phe				
1430		1435		1440
Leu Lys Glu Tyr Arg Leu Leu Lys Gln Ala Ile Lys Asp Glu Thr				
1445		1450		1455
Gly Ser Leu Leu Pro Ser Pro Asp Tyr Asn Gln Asn Ser Ile Ala				
1460		1465		1470
Ser Cys His His Ser Gln Glu Gln Leu Ala Leu Val Glu Glu Ser				
1475		1480		1485
Pro Ala Asp Asn Met Leu Ala Ala Ser Leu Phe Pro Gly Gly Pro				
1490		1495		1500
Ser Gly Arg Asp His Val Val Leu Thr Gly Ser Ala Gly Pro Lys				
1505		1510		1515
Glu Leu Trp Glu Met Val Trp Glu His Gly Ala Tyr Val Leu Val				
1520		1525		1530
Ser Leu Gly Leu Pro Asp Thr Lys Glu Lys Pro Gln Asp Ile Trp				
1535		1540		1545
Pro Met Glu Met Gln Pro Ile Val Thr Asp Met Val Thr Val His				
1550		1555		1560
Arg Val Ala Glu Ser Asn Thr Ala Gly Trp Pro Ser Thr Leu Ile				
1565		1570		1575
Arg Val Ile His Gly Asp Ser Gly Thr Glu Arg Gln Val Gln Cys				
1580		1585		1590
Leu Gln Phe Pro His Cys Glu Thr Gly Ser Glu Leu Pro Ala Asn				
1595		1600		1605
Thr Leu Leu Thr Phe Leu Asp Ala Val Gly Gln Cys Cys Ser Arg				
1610		1615		1620
Gly Asn Ser Lys Lys Pro Gly Thr Leu Leu Ser His Ser Ser Lys				
1625		1630		1635
Val Thr Asn Gln Leu Ser Thr Phe Leu Ala Met Glu Gln Leu Leu				
1640		1645		1650
Gln Gln Ala Gly Thr Glu Arg Thr Val Asp Val Phe Ser Val Ala				

1555	1560	1565
Leu Lys Gln Thr Gln Ala Cys Gly Leu Lys Thr Pro Thr Leu Glu		
1570	1575	1580
Gln Tyr Ile Tyr Leu Tyr Asn Cys Leu Asn Ser Ala Leu Arg Asn		
1585	1590	1595
Arg Leu Pro Arg Ala Arg Lys		
1700	1705	
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Leu Ala Glu Asp Asp Ala Cys Ser Ser Leu Gly Gly Ser Pro Asp Arg		
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Gln Gly Gly Gly Pro Leu Leu Ser Val Asn Val Ser Ser His Gly Lys		
	35	40 45
Ser Thr Ser Leu Phe Leu Ser Trp Val Ala Ala Glu Leu Gly Gly Phe		
	50	55 60
Asp Tyr Ala Leu Ser Leu Arg Ser Val Asp Ser Ser Gly Ser Pro Glu		
65	70	75 80
Gly Gln Gln Leu Gln Ala His Thr Asn Glu Ser Gly Phe Glu Phe His		
	85	90 95
Gly Leu Val Pro Gly Ser Arg Tyr Gln Leu Lys Leu Thr Val Leu Arg		
	100	105 110
Pro Cys Trp Gln Asn Val Thr Ile Thr Leu Thr Ala Arg Thr Ala Pro		
	115	120 125
Thr Val Val Arg Gly Leu Gln Leu His Ser Ala Gly Ser Pro Ala Arg		
	130	135 140
Leu Glu Ala Ser Trp Ser Asp Ala Pro Gly Asp Gln Asp Ser Tyr Gln		
145	150	155 160
Leu Leu Leu Tyr His Leu Glu Ser Gln Thr Leu Ala Cys Asn Val Ser		
	165	170 175
Val Ser Pro Asp Thr Leu Ser Tyr Ser Phe Gly Asp Leu Leu Pro Gly		
	180	185 190
Thr Gln Tyr Val Leu Glu Val Ile Thr Trp Ala Gly Ser Leu His Ala		
	195	200 205

Lys	Thr	Ser	Ile	Leu	Gln	Trp	Thr	Glu	Pro	Val	Pro	Pro	Asp	His	Leu	210	215	220
Ala	Leu	Arg	Ala	Leu	Gly	Thr	Ser	Ser	Leu	Gln	Ala	Phe	Trp	Asn	Ser	225	230	235
Ser	Glu	Gly	Ala	Thr	Ser	Phe	His	Leu	Met	Leu	Thr	Asp	Leu	Leu	Gly	245	250	255
Gly	Thr	Asn	Thr	Thr	Ala	Val	Ile	Arg	Gln	Gly	Val	Ser	Thr	His	Thr	260	265	270
Phe	Leu	His	Leu	Ser	Pro	Gly	Thr	Pro	His	Glu	Leu	Lys	Ile	Cys	Ala	275	280	285
Ser	Ala	Gly	Pro	His	Gln	Ile	Trp	Gly	Pro	Ser	Ala	Thr	Glu	Trp	Thr	290	295	300
Tyr	Pro	Ser	Tyr	Pro	Ser	Asp	Leu	Val	Leu	Thr	Pro	Leu	Arg	Asn	Glu	305	310	315
Leu	Trp	Ala	Ser	Trp	Lys	Ala	Gly	Leu	Gly	Ala	Arg	Asp	Gly	Tyr	Val	320	325	330
Leu	Lys	Leu	Ser	Gly	Pro	Met	Glu	Ser	Thr	Ser	Thr	Leu	Gly	Pro	Glu	335	340	345
Glu	Cys	Asn	Ala	Val	Phe	Pro	Gly	Pro	Leu	Pro	Pro	Gly	His	Tyr	Thr	350	355	360
Leu	Gln	Leu	Lys	Val	Leu	Ala	Gly	Pro	Tyr	Asp	Ala	Trp	Val	Glu	Gly	365	370	375
Ser	Thr	Trp	Leu	Ala	Glu	Ser	Ala	Ala	Leu	Pro	Arg	Glu	Val	Pro	Gly	380	385	390
Ala	Arg	Leu	Trp	Leu	Asp	Gly	Leu	Glu	Ala	Ser	Lys	Gln	Pro	Gly	Arg	395	400	405
Arg	Ala	Leu	Leu	Tyr	Ser	Asp	Asp	Ala	Pro	Gly	Ser	Leu	Gly	Asn	Ile	410	415	420
Ser	Val	Pro	Ser	Gly	Ala	Thr	His	Val	Ile	Phe	Cys	Gly	Leu	Val	Pro	425	430	435
Gly	Ala	His	Tyr	Arg	Val	Asp	Ile	Ala	Ser	Ser	Thr	Gly	Asp	Ile	Ser	440	445	450
Gln	Ser	Ile	Ser	Gly	Tyr	Thr	Ser	Pro	Leu	Pro	Pro	Gln	Ser	Leu	Glu	455	460	465
Val	Ile	Ser	Arg	Ser	Ser	Pro	Ser	Asp	Leu	Thr	Ile	Ala	Trp	Gly	Pro	470	475	480
Ala	Pro	Gly	Gln	Leu	Glu	Gly	Tyr	Lys	Val	Thr	Trp	His	Gln	Asp	Gly	485	490	495
																500	505	510

Ser Gln Arg Ser Pro Gly Asp Leu Val Asp Leu Gly Pro Asp Thr Leu  
 515 520 525  
 Ser Leu Thr Leu Lys Ser Leu Val Pro Gly Ser Ser Tyr Thr Val Ser  
 530 535 540  
 Ala Trp Ala Trp Ala Gly Asn Leu Gly Ser Asp Ser Gln Lys Ile His  
 545 550 555 560  
 Ser Cys Thr Arg Pro Ala Pro Pro Thr Asn Leu Ser Leu Gly Phe Ala  
 565 570 575  
 His Gln Pro Ala Ala Leu Lys Ala Ser Trp Tyr His Pro Pro Gly Gly  
 580 585 590  
 Arg Asp Ala Phe His Leu Arg Leu Tyr Arg Leu Arg Pro Leu Thr Leu  
 595 600 605  
 Glu Ser Glu Lys Val Leu Pro Arg Glu Ala Gln Asn Phe Ser Trp Ala  
 610 615 620  
 Gln Leu Thr Ala Gly Cys Glu Phe Gln Val Gln Leu Ser Thr Leu Trp  
 625 630 635 640  
 Gly Ser Glu Arg Ser Ser Ser Ala Asn Ala Thr Gly Trp Thr Pro Pro  
 645 650 655  
 Ser Ala Pro Thr Leu Val Asn Val Thr Ser Asp Ala Pro Thr Gln Leu  
 660 665 670  
 Gln Val Ser Trp Ala His Val Pro Gly Gly Arg Ser Arg Tyr Gln Val  
 675 680 685  
 Thr Leu Tyr Gln Glu Ser Thr Arg Thr Ala Thr Ser Ile Met Gly Pro  
 690 695 700  
 Lys Glu Asp Gly Thr Ser Phe Leu Gly Leu Thr Pro Gly Thr Lys Tyr  
 705 710 715 720  
 Lys Val Glu Val Ile Ser Trp Ala Gly Pro Leu Tyr Thr Ala Ala Ala  
 725 730 735  
 Asn Val Ser Ala Trp Thr Tyr Pro Leu Ile Pro Asn Glu Leu Leu Val  
 740 745 750  
 Ser Met Gln Ala Gly Ser Ala Val Val Asn Leu Ala Trp Pro Ser Gly  
 755 760 765  
 Pro Leu Gly Gln Gly Ala Cys His Ala Gln Leu Ser Asp Ala Gly His  
 770 775 780  
 Leu Ser Trp Glu Gln Pro Leu Lys Leu Gly Gln Glu Leu Phe Met Leu  
 785 790 795 800  
 Arg Asp Leu Thr Pro Gly His Thr Ile Ser Met Ser Val Arg Cys Arg  
 805 810 815



Ala Gly Pro Leu Gln Ala Ser Thr His Leu Val Val Leu Ser Val Glu	820	825	830
Pro Gly Pro Val Glu Asp Val Leu Cys His Pro Glu Ala Thr Tyr Leu	835	840	845
Ala Leu Asn Trp Thr Met Pro Ala Gly Asp Val Asp Val Cys Leu Val	850	855	860
Val Val Glu Arg Leu Val Pro Gly Gly Gly Thr His Phe Val Phe Gln	865	870	875
Val Asn Thr Ser Gly Asp Ala Leu Leu Leu Pro Asn Leu Met Pro Thr	885	890	895
Thr Ser Tyr Arg Leu Ser Leu Thr Val Leu Gly Arg Asn Ser Arg Trp	900	905	910
Ser Arg Ala Val Ser Leu Val Cys Ser Thr Ser Ala Glu Ala Trp His	915	920	925
Pro Pro Glu Leu Ala Glu Pro Pro Gln Val Glu Leu Gly Thr Gly Met	930	935	940
Gly Val Thr Val Met Arg Gly Met Phe Gly Lys Asp Asp Gly Gln Ile	945	950	955
Gln Trp Tyr Gly Ile Ile Ala Thr Ile Asn Met Thr Leu Ala Gln Pro	965	970	975
Ser Arg Glu Ala Ile Asn Tyr Thr Trp Tyr Asp His Tyr Tyr Arg Gly	980	985	990
Cys Glu Ser Phe Leu Ala Leu Leu Phe Pro Asn Pro Phe Tyr Pro Glu	995	1000	1005
Pro Trp Ala Gly Pro Arg Ser Trp Thr Val Pro Val Gly Thr Glu	1010	1015	1020
Asp Cys Asp Asn Thr Gln Glu Ile Cys Asn Gly Arg Leu Lys Ser	1025	1030	1035
Gly Phe Gln Tyr Arg Phe Ser Val Val Ala Phe Ser Arg Leu Asn	1040	1045	1050
Thr Pro Glu Thr Ile Leu Ala Phe Ser Ala Phe Ser Glu Pro Arg	1055	1060	1065
Ala Ser Ile Ser Leu Ala Ile Ile Pro Leu Thr Val Met Leu Gly	1070	1075	1080
Ala Val Val Gly Ser Ile Val Ile Val Cys Ala Val Leu Cys Leu	1085	1090	1095
Leu Arg Trp Arg Cys Leu Lys Gly Pro Arg Ser Glu Lys Asp Gly	1100	1105	1110

Phe	Ser	Lys	Glu	Leu	Met	Pro	Tyr	Asn	Leu	Trp	Arg	Thr	His	Arg	
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Pro	Ile	Pro	Ile	His	Ser	Phe	Arg	Gln	Ser	Tyr	Glu	Ala	Lys	Ser	
1130						1135					1140				
Ala	His	Ala	His	Gln	Thr	Phe	Phe	Gln	Glu	Phe	Glu	Glu	Leu	Lys	
1145						1150					1155				
Glu	Val	Gly	Lys	Asp	Gln	Pro	Arg	Leu	Glu	Ala	Glu	His	Pro	Asp	
1150						1155					1170				
Asn	Ile	Ile	Lys	Asn	Arg	Tyr	Pro	His	Val	Leu	Pro	Tyr	Asp	His	
1175						1180					1185				
Ser	Arg	Val	Arg	Leu	Thr	Gln	Leu	Pro	Gly	Glu	Pro	His	Ser	Asp	
1190						1195					1200				
Tyr	Ile	Asn	Ala	Asn	Phe	Ile	Pro	Gly	Tyr	Ser	His	Thr	Gln	Glu	
1205						1210					1215				
Ile	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Lys	Lys	Thr	Leu	Glu	Asp	Phe	
1220						1225					1230				
Trp	Arg	Leu	Val	Trp	Glu	Gln	Gln	Val	His	Val	Ile	Ile	Met	Leu	
1235						1240					1245				
Thr	Val	Gly	Met	Glu	Asn	Gly	Arg	Val	Leu	Cys	Glu	His	Tyr	Trp	
1250						1255					1260				
Pro	Ala	Asn	Ser	Thr	Pro	Val	Thr	His	Gly	His	Ile	Thr	Ile	His	
1265						1270					1275				
Leu	Leu	Ala	Glu	Glu	Pro	Glu	Asp	Glu	Trp	Thr	Arg	Arg	Glu	Phe	
1280						1285					1290				
Gln	Leu	Gln	His	Gly	Thr	Glu	Gln	Lys	Gln	Arg	Arg	Val	Lys	Gln	
1295						1300					1305				
Leu	Gln	Phe	Thr	Thr	Trp	Pro	Asp	His	Ser	Val	Pro	Glu	Ala	Pro	
1310						1315					1320				
Ser	Ser	Leu	Leu	Ala	Phe	Val	Glu	Leu	Val	Gln	Glu	Gln	Val	Gln	
1325						1330					1335				
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1355						1360					1365				
Gln	Leu	Glu	Glu	Glu	Lys	Val	Ala	Asp	Val	Phe	Asn	Thr	Val	Tyr	
1370						1375					1380				
Ile	Leu	Arg	Leu	His	Arg	Pro	Leu	Met	Ile	Gln	Thr	Leu	Ser	Gln	
1385						1390					1395				

Tyr	Ile	Phe	Leu	His	Ser	Cys	Leu	Leu	Asn	Lys	Ile	Leu	Glu	Gly
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1445						1450					1455			
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1460						1465					1470			
Ser	Arg	Arg	His	Ser	Gln	Glu	Gln	Phe	Ala	Leu	Val	Glu	Glu	Cys
1475						1480					1485			
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Glu	Leu	Trp	Glu	Met	Val	Trp	Glu	His	Asp	Ala	His	Val	Leu	Val
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Ser	Leu	Gly	Leu	Pro	Asp	Thr	Lys	Glu	Lys	Pro	Pro	Asp	Ile	Trp
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Pro	Val	Glu	Met	Gln	Pro	Ile	Val	Thr	Asp	Met	Val	Thr	Val	His
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Cys	Leu	Gln	Phe	Pro	Cys	Ser	Glu	Ser	Gly	Cys	Glu	Leu	Pro	Ala
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Lys	Asn	Thr	Asn	Gln	Leu	Gly	Thr	Phe	Leu	Ala	Met	Glu	Gln	Leu
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Leu	Gln	Gln	Ala	Gly	Thr	Glu	Arg	Thr	Val	Asp	Val	Phe	Asn	Val
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<400> 39

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Ile Cys Cys Ser Lys Leu Val Lys Arg Arg Leu Gln Gln Gly Lys Val  
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Thr Glu Pro Gln Asp Val Val Val Tyr Asp Gln Ser Thr Arg Asp Ala  
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Ser Val Leu Ala Ala Asp Ser Phe Leu Ser Ile Leu Leu Ser Lys Leu  
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Asp Gly Cys Phe Asp Ser Val Ala Ile Leu Thr Gly Gly Phe Ala Thr  
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Phe Ser Ser Cys Phe Pro Gly Leu Cys Glu Gly Lys Pro Ala Ala Leu  
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Leu Pro Met Ser Leu Ser Gln Pro Cys Leu Pro Val Pro Ser Val Gly  
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Leu Thr Arg Ile Leu Pro His Leu Tyr Leu Gly Ser Gln Lys Asp Val  
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Leu Asn Lys Asp Leu Met Thr Gln Asn Gly Ile Ser Tyr Val Leu Asn  
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Ala Ser Asn Ser Cys Pro Lys Pro Asp Phe Ile Cys Glu Ser Arg Phe  
 195 200 205

Met Arg Val Pro Ile Asn Asp Asn Tyr Cys Glu Lys Leu Leu Pro Trp  
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Leu Asp Lys Ser Ile Glu Phe Ile Asp Lys Ala Lys Leu Ser Ser Cys  
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Gln Val Ile Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile  
 245 250 255  
 Ala Ile Ala Tyr Ile Met Lys Thr Met Gly Met Ser Ser Asp Asp Ala  
 260 265 270  
 Tyr Arg Phe Val Lys Asp Arg Arg Pro Ser Ile Ser Pro Asn Phe Asn  
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 Phe Leu Gly Gln Leu Leu Glu Tyr Glu Arg Thr Leu Lys Leu Leu Ala  
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 Ala Leu Gln Gly Asp Pro Gly Thr Pro Ser Gly Thr Pro Glu Pro Pro  
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 Ser Glu Ser Ala Ala Thr Gly Asn Ala Ala Ala Arg Glu Gly Gly Leu  
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 Ala Tyr Ala Pro Ser Arg Arg Pro Asp Gly Pro Gly Pro Pro Asp Pro  
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 Pro Gly Pro Gly Gln Pro Ala Gly Pro Gly Ala Trp Ala Pro Pro Leu  
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580 585 590

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Ser  
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Ile Cys Cys Ser Lys Leu Val Lys Arg Arg Leu Gln Gln Gly Lys Val  
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Thr Ile Ala Glu Leu Ile Gln Pro Ala Thr Arg Ser Gln Val Asp Ala  
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Thr Glu Pro Gln Asp Val Val Val Tyr Asp Gln Ser Thr Arg Asp Ala  
85 90 95

Ser Val Leu Ala Ala Asp Ser Phe Leu Ser Ile Leu Leu Ser Lys Leu  
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Asp Gly Cys Phe Asp Ser Val Ala Ile Leu Thr Gly Gly Phe Ala Thr  
115 120 125

Phe Ser Ser Cys Phe Pro Gly Leu Cys Glu Gly Lys Pro Ala Thr Leu  
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Pro Ser Met Ser Leu Ser Gln Pro Cys Leu Pro Val Pro Ser Val Gly  
145 150 155 160

Leu Thr Arg Ile Leu Pro His Leu Tyr Leu Gly Ser Gln Lys Asp Val

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Tyr	Arg	Phe	Val	Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn				
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Ser	Pro	Ser	Ala	Gly	Gly	Asp	Ala	Pro	Ile	Pro	Ser	Thr	Ala	Pro	Ala				
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<400> 42

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Lys	Glu	Leu	Met	Gln	Gln	Asn	Gly	Ile	Gly	Tyr	Val	Leu	Asn	Ala	Ser	
180					185					190						
Asn	Thr	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Pro	Glu	Ser	His	Phe	Leu	Arg	
195					200					205						
Val	Pro	Val	Asn	Asp	Ser	Phe	Cys	Glu	Lys	Ile	Leu	Pro	Trp	Leu	Asp	
210					215					220						
Lys	Ser	Val	Asp	Phe	Ile	Glu	Lys	Ala	Lys	Ala	Ser	Asn	Gly	Cys	Val	
225					230					235					240	
Leu	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	Ala	Ile	
245					250					255						
Ala	Tyr	Ile	Met	Lys	Arg	Met	Asp	Met	Ser	Leu	Asp	Glu	Ala	Tyr	Arg	
260					265					270						
Phe	Val	Lys	Glu	Lys	Arg	Pro	Thr	Ile	Ser	Pro	Asn	Phe	Asn	Phe	Leu	
275					280					285						
Gly	Gln	Leu	Leu	Ala	Tyr	Glu	Lys	Lys	Ile	Lys	Asn	Gln	Thr	Gly	Ala	
290					295					300						
Ser	Gly	Pro	Lys	Ser	Lys	Leu	Lys	Leu	Leu	Pro	Leu	Glu	Lys	Pro	Asn	
305					310					315					320	
Glu	Pro	Val	Pro	Ala	Val	Ser	Glu	Gly	Gly	Gln	Lys	Ser	Glu	Thr	Pro	

325										330					335				
Leu	Ser	Pro	Pro	Cys	Ala	Asp	Ser	Ala	Thr	Ser	Glu	Ala	Ala	Gly	Gln				
			340					345					350						
Arg	Pro	Val	His	Pro	Ala	Ser	Val	Pro	Ser	Val	Pro	Ser	Val	Gln	Pro				
		355					360					365							
Ser	Leu	Leu	Glu	Asp	Ser	Pro	Leu	Val	Gln	Ala	Leu	Ser	Gly	Leu	His				
	370					375					380								
Leu	Ser	Ala	Asp	Arg	Leu	Glu	Asp	Ser	Asn	Lys	Leu	Lys	Arg	Ser	Phe				
385					390				395						400				
Ser	Leu	Asp	Ile	Lys	Ser	Val	Ser	Tyr	Ser	Ala	Ser	Met	Ala	Ala	Ser				
			405					410						415					
Leu	His	Gly	Phe	Ser	Ser	Ser	Glu	Asp	Ala	Leu	Glu	Tyr	Tyr	Lys	Pro				
		420					425						430						
Ser	Thr	Thr	Leu	Asp	Gly	Thr	Asn	Lys	Leu	Cys	Gln	Phe	Ser	Pro	Val				
		435					440					445							
Gln	Glu	Leu	Ser	Glu	Gln	Thr	Pro	Glu	Thr	Ser	Pro	Asp	Lys	Glu	Glu				
	450					455					460								
Ala	Ser	Ile	Pro	Lys	Lys	Leu	Gln	Thr	Ala	Arg	Pro	Ser	Asp	Ser	Gln				
465					470				475						480				
Ser	Lys	Arg	Leu	His	Ser	Val	Arg	Thr	Ser	Ser	Ser	Gly	Thr	Ala	Gln				
			485					490						495					
Arg	Ser	Leu	Leu	Ser	Pro	Leu	His	Arg	Ser	Gly	Ser	Val	Glu	Asp	Asn				
		500						505					510						
Tyr	His	Thr	Ser	Phe	Leu	Phe	Gly	Leu	Ser	Thr	Ser	Gln	Gln	His	Leu				
	515						520					525							
Thr	Lys	Ser	Ala	Gly	Leu	Gly	Leu	Lys	Gly	Trp	His	Ser	Asp	Ile	Leu				
	530				535						540								
Ala	Pro	Gln	Thr	Ser	Thr	Pro	Ser	Leu	Thr	Ser	Ser	Trp	Tyr	Phe	Ala				
545					550				555					560					
Thr	Glu	Ser	Ser	His	Phe	Tyr	Ser	Ala	Ser	Ala	Ile	Tyr	Gly	Gly	Ser				
			565					570					575						
Ala	Ser	Tyr	Ser	Ala	Tyr	Ser	Cys	Ser	Gln	Leu	Pro	Thr	Cys	Gly	Asp				
		580					585						590						
Gln	Val	Tyr	Ser	Val	Arg	Arg	Arg	Gln	Lys	Pro	Ser	Asp	Arg	Ala	Asp				
	595						600					605							
Ser	Arg	Arg	Ser	Trp	His	Glu	Glu	Ser	Pro	Phe	Glu	Lys	Gln	Phe	Lys				
	610				615						620								
Arg	Arg	Ser	Cys	Gln	Met	Glu	Phe	Gly	Glu	Ser	Ile	Met	Ser	Glu	Asn				

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Gly Ser Met Glu Ile Ile Glu Val Ser
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<210> 44  
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 <212> DNA  
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<400> 44  
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<210> 45  
 <211> 36  
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 aggatagtag taagagacgc 80

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<400> 46  
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<210> 47  
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<400> 47  
 ctgttcgac aagccctg 18

<210> 48  
 <211> 80

<212> DNA  
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 aggatagtag taagagacgc 80  
  
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 tcccgccagc cggcccggg 79  
  
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 cagctgtcgc tgtgaggg 18  
  
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<211> 30  
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 gnggcgcgjc agcgccagtc 80  
  
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 ttaagttctt gtaagaatct 80  
  
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 <210> 59  
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 <400> 59  
 aacctggatg cttcccttct 20



<210> 60  
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 cagcccagac tggaggctga 30  
  
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 <400> 64  
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 <400> 65  
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<210> 65  
 <211> 80  
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 <213> HOMO SAPIENS

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 ctatcagcga gaactgttaa 30

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<400> 67  
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<210> 68  
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 <212> DNA  
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<400> 68  
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<210> 69  
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<400> 69  
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<210> 70  
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<400> 70  
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<400> 71  
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<210> 72  
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<400> 72  
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<210> 73  
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<400> 73  
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 cagatcagac tggaggctga 30

<210> 74  
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<400> 74  
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 aaagcttgt ggcctgagc 30

<210> 75  
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 <212> PRT  
 <213> bacteriophage T7

<400> 75

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 76  
 <211> 733  
 <212> DNA  
 <213> homo sapiens

<400> 76  
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 aattcgaggg tgcaccgtca gtcttctctt tcccccaaa acccaaggac acctcatga 100  
 tctcccgga tctgagggtc acatgggtgg tggtagcgt aagccacgaa gacctgagg 150  
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 200  
 aggagcagta caacagcagc tacctgtgtg tcaggtctct caccgtctg caccaggact 250

gggtgaatgg caaggagtag aagtgcagg tctccaacaa agcctccca accccatcg 360  
 agaaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac acctgcccc 420  
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgectggto aaaggcttct 480  
 atccaagoga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540  
 ccangcctcc cgtgctggac tccgaaggct ccttcttct ctacagcaag ctcacgtgg 600  
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcac gaggctctgc 660  
 acaaccacta caccgagaag agcctctccc tgtctccggg taaatgagtg cgaaggccgc 720  
 gactctagag gat 733

<210> 77  
 <211> 7  
 <212> PRT  
 <213> HOMO SAPIENS

<400> 77

Asp Tyr Ile Asn Ala Ser Asn  
 1 5

<210> 78  
 <211> 6  
 <212> PRT  
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<220>  
 <221> VARIANT  
 <222> (2)..(2)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> VARIANT  
 <222> (3)..(3)  
 <223> wherein 'Xaa' is any amino acid.

<400> 78

Cys Xaa Xaa Tyr Trp Pro  
 1 5

<210> 79  
 <211> 9  
 <212> PRT  
 <213> HOMO SAPIENS

<220>  
 <221> Variant  
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<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (6)..(6)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (7)..(7)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (8)..(8)

<223> wherein 'Xaa' is any amino acid.

<400> 79

Ile Val Val Met Xaa Xaa Xaa Xaa Glu  
1 5

<210> 80

<211> 8

<212> PPT

<213> HOMO SAPIENS

<400> 80

Asp Asn Tyr Ile Asn Ala Ser Asn  
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<210> 81

<211> 6

<212> PPT

<213> HOMO SAPIENS

<220>

<221> Variant

<222> (2)..(2)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (3)..(3)

<223> wherein 'Xaa' is any amino acid.

<400> 81

Cys Xaa Xaa Tyr Trp Pro  
1 5

<210> 82  
 <211> 9  
 <212> PRT  
 <213> HOMO SAPIENS

<220>  
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 <223> wherein 'Xaa' is any amino acid.

<220>  
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 <223> wherein 'Xaa' is any amino acid.

<220>  
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 <222> (7)..(7)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (8)..(8)  
 <223> wherein 'Xaa' is any amino acid.

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 1 5

<210> 83  
 <211> 511  
 <212> DNA  
 <213> homo sapiens

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 ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180  
 ggaagcatcc aggttccgga ctggcctttt gatgatggta cagcaccatc cagccagata 240  
 attgataact ggtaaact tatgaaaaat aaatttcattg aagatcctgg ttgttgatt 300  
 gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgcc tagctttaat 360  
 tgaagggtgga atgaaatatg aaaatgtagt acagttcatc agataaaagt gacatggaac 420  
 ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgacact 480

cagaaatccc agaaataact gtttccttca g

511

<210> 84  
<211> 157  
<212> PRT  
<213> homo sapiens

<400> 84

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Val Arg Phe Leu Ile Thr His Asn Pro Thr Asn Thr Tyr Phe Asn Arg  
20 25 30  
Phe Leu Gln Glu Leu Lys Gln Asp Gly Val Thr Thr Ile Val Arg Val  
35 40 45  
Lys Ala Thr Tyr Asn Ile Ala Leu Leu Glu Lys Gly Ser Ile Gln Val  
50 55 60  
Pro Asp Trp Pro Phe Asp Asp Gly Thr Ala Pro Ser Ser Gln Ile Ile  
65 70 75 80  
Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro Gly  
85 90 95  
Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Glu Leu Gln Leu  
100 105 110  
Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asn Val  
115 120 125  
Val Gln Phe Ile Arg Lys His Gly Thr Phe Asn Ser Lys Gln Leu Leu  
130 135 140  
Tyr Leu Glu Lys Tyr Cys Leu Lys Ile Cys Leu His Leu Arg Asn Pro  
145 150 155 160  
Arg Asn Asn Cys Phe Leu Gln  
165

<210> 85  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 85

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile  
1 5 10

<210> 86  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 85

Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg  
1 5 10

<210> 37

<211> 14

<212> PRT

<213> homo sapiens

<400> A7

Ile Gly Tyr Val Leu Asn Ala Ser Asn Thr Cys Pro Lys Pro  
1 5 10

<210> 14

<211> 14

<212> PRT

<213> homo sapiens

<400> 44

Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu  
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<210> 89

<211> 14

<212> PRT

<213> homo sapiens

<400> 87

Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys  
1 5 10

<210> 98

<211> 14

<212> PRT

<213> homo sapiens

<400> 98

Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys  
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<210> 91

<211> 13

<212> PRT

<213> homo sapiens

<400> 91

Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu  
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<210> 92



<211> 12  
<212> PPT  
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<400> 91

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1 5 10

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<400> 93

Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile  
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<210> 94  
<211> 13  
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<400> 94

Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp  
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<211> 13  
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<400> 95

Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
1 5 10

<210> 96  
<211> 13  
<212> PPT  
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<400> 96

Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser  
1 5 10

<210> 97  
<211> 13  
<212> PPT  
<213> homo sapiens

<400> 97

Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln



<400> 103

Asn Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala  
1 5 10 15

Thr Ile Ala Ile Ala Tyr Ile  
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<210> 104

<211> 39

<212> DNA

<213> Homo sapiens

<400> 104

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<210> 105

<211> 37

<212> DNA

<213> Homo sapiens

<400> 105

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<210> 106

<211> 39

<212> DNA

<213> Homo sapiens

<400> 106

gcagcagcgg ccgcatggcc catgagatga ttggaactc 39

<210> 107

<211> 37

<212> DNA

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<400> 107

gcagcagtcg acctgcacgc tgggcacgct gggcacg 37

<210> 108

<211> 5450

<212> DNA

<213> Homo sapiens

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<400> 108

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gtgacaactt tegtttccct ctgaggggaat tgggaggtcg ggggccccaa aagctttcag	180
tccagtgtaa agctgttggg gggggggagc aaaggtaaag aatgatgtaa tgcgctggct	240
gctccaaagc atcttttgtt gtggaatggg tattccagtc atctctttat gaatcaaag	300
tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga	360
gacattcact tggagggctc ttgtgaaaa tgggtttaac tctcttttg ccagtcacca	420
ccagcctgac ctcatacact tttagtacaa tggagtggct gagcctttga gcacaccacc	480
attacatcat cgtggcaaat taaagaagga ggtgggaaaa gaggacttat tgttgtc	537
atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg	595
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val	
1 5 10 15	
gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg	633
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg	
20 25 30	
cca ttt gtg gaa tac aat aca tcc cac att ttg gaa gcc att aat atc	691
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile	
35 40 45	
aac tgc tcc aag ctt atg aag cga agg ttg caa cag gac aaa gtg tta	729
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu	
50 55 60	
att aca gag ctc atc cag cat tca gcg aaa cat aag gtt gac att gat	777
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp	
65 70 75 80	
tgc agt cag aag gtt gta gtt tac gat caa agc tcc caa gat gtt gcc	825
Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala	
85 90 95	
tct ctc tct tca gac tgt ttt ctc act gta ctt ctg ggt aaa ctg gag	873
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu	
100 105 110	
aag agc ttc aac tct gtt cac ctg ctt gca ggt ggg ttt gct gag ttc	921
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe	
115 120 125	
tct cgt tgt ttc cct ggc ctc tgt gaa gga aaa tcc act cta gtc cct	959
Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro	
130 135 140	
acc tgc att tct cag cct tgc tta cct gtt gcc aac att ggg cca acc	1017
Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr	
145 150 155 160	
cga att ctt ccc aat ctt tat ctt ggc tgc cag cga gat gtc ctc aac	1055
Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn	

165	170	175	
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tat acc tgt cca aag cct gac ttt atc ccc gag tct cat ttc ctg cgt Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg 195 200 205			1161
gtg cct gtg aat gac agc ttt tgt gag aaa att ttg ccg tgg ttg gac Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp 210 215 220			1209
aaa tca gta gat ttc att gag aaa gca aaa gcc tcc aat gga tgt gtt Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val 225 230 235 240			1257
cta gtg cac tgt tta gct ggg atc tcc cgc tcc gcc acc atc gct atc Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile 245 250 255			1305
gcc tac atc atg aag agg atg gac atg tct tta gat gaa gct tac aga Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg 260 265 270			1353
ttt gtg aaa gaa aaa aga cct act ata tct cca aac ttc aat ttt ctg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu 275 280 285			1401
ggc caa ctc ctg gac tat gag aag aag att aag aac cag act gga gca Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala 290 295 300			1449
tca ggg cca aag agc aaa ctc aag ctg ctg cac ctg gag aag cca aat Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn 305 310 315 320			1497
gaa cct gtc cct gct gtc tca gag ggt gga cag aaa agc gag acg ccc Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro 325 330 335			1545
ctc agt cca ccc tgt gcc gac tct gct acc tca gag gca gca gga caa Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln 340 345 350			1593
agg ccc gtg cat ccc gcc agc gtg ccc agc gtg ccc agc gtg cag ccg Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro 355 360 365			1641
tcg ctg tta gag gac agc ccg ctg gta cag gcg ctc agt ggg ctg cac Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His 370 375 380			1689
ctg tcc gca gac agg ctg gaa gac agc aat aag ctc aag cgt tcc ttc Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe 385 390 395 400			1737

tct ctg gat atc aaa tca gtt tca tat tca gcc agc atg gca gca tcc Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser 405 410 415	1785
tta cat ggc ttc tcc tca tca gaa gat gct ttg gaa tac tac aaa cct Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro 420 425 430	1833
tcc act act ctg gat ggg acc aac aag cta tgc cag ttc tcc cct gtt Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val 435 440 445	1881
cag gaa cta tgc gag cag act ccc gaa acc agt cct gat aag gag gaa Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu 450 455 460	1929
gcc agc atc ccc aag aag ctg cag acc gcc agg cct tca gac agc cag Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln 465 470 475 480	1977
agc aag cga ttg cat tgc gtc aga acc agc agc agt ggc acc gcc cag Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln 485 490 495	2025
agg tcc ctt tta tct cca ctg cat cga agt ggg agc gtg gag gac aat Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn 500 505 510	2073
tac cac acc agc ttc ctt ttc ggc ctt tcc acc agc cag cag cac ctc Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu 515 520 525	2121
acg aag tct gct ggc ctg ggc ctt aag ggc tgg cac tgc gat atc ttg Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu 530 535 540	2169
gcc ccc cag acc tct acc cct tcc ctg acc agc agc tgg tat ttt gcc Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala 545 550 555 560	2217
aca gag tcc tca cac ttc tac tct gcc tca gcc atc tac gga ggc agt Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser 565 570 575	2265
gcc agt tac tct gcc tac agc tgc agc cag ctg ccc act tgc gga gac Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp 580 585 590	2313
caa gtc tat tct gtg cgc agg cgg cag aag cca agt gac aga gct gac Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp 595 600 605	2361
tgc cgg cgg agc tgg cat gaa gag agc ccc ttt gaa aag cag ttt aaa Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys 610 615 620	2409

[illegible]

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tcttggcagc tgaacatagg aggtcactgg aacaagtgat agtgcagatt ggttttcaaa	4052
catactcttg gcttgagttt tatcagctac aatgtgggtc ctcttttgaa gctttaattc	4112
acaacagcag ctttttgggg gtgggggtgg gcgggtgttg tcattgttct ttccttctct	4172
gtaagtgtcg ctagtgtctg cctcgtatct cagggtttttc tctgtttttg agaaatggac	4232
agttttttga ccaggatgtg acttcagtgt tcctatgggtg acttctaaaa ccagcacaga	4292
atgatatgac tcaacacaga ccgacttggg tatgggggatg atgagccgca cagacctcac	4352
tagttgtgca caaataatgt gctatgatgg ggtgtaaagt gaaggcagaa gagggtcagc	4412
cgcattgtta tgatactggg aaagtgctgg tcaacgattt gagttagttt ttagatatac	4472
attgaaatct ttaatcagac attctcaagt ttcacacagt agtttttgat gttatgtaca	4532
cacacaccaa atgtgtaaca gttcaccact tccagagtgt ggtcatgccc aaaacatgtt	4592
taagaaagga aagcagtagc tcttgctaa cgatgtttca ggaggtttg ggcaacttggg	4652
tttaatgagc ttctgtcatt tagggcttct cttggccatg gtcccccttc ttctggaact	4712
gtgatgtagt cacatcctac agcctttagt gctggttcac tagtgtcaga taatcagttc	4772
ttggaatcga gactgccgtg gcgaaggggt ggcctcggag gcaggctctg gagctgcttg	4832
gatgtcttta ggtgggggtg tggtcggctc tcttcagcat gtaattgggg aaacctcgc	4892
gtctactagg ggtgatacag atggtgattt taaagagcaa aactagactt ctatgtgaga	4952
agtgtcggaa aatgatttag gacatgtgta aagttagatg gaaagactgt aaatgtttaa	5012
tatgaatata gtgttctttt gaagtaaggc cagctgttga acggttaaac tgtgcatttc	5072
tcattttgat gtgtcatgta tgttaatgta tgaaatgatt aaataaaatc aaaactggta	5132
cctgtttata cataaatacg agaaaagacc tatctttgca gccataaact cgggtgggac	5192
accaccactc aagttgccaa aggaggcagt ggtgaaacct gtctgttct cacttaaatg	5252
aggatttagc tcaaaataaa gtggtggtgt catcaggttt attccgtgtt ctgtcattca	5312
catggaaac cgatgatta gctaacagtt tagtgccagc cttcattctt tactgtgtac	5372
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gattccagaa cacacaag	5450

<210> 109  
 <211> 665  
 <212> PRT



<213> Homo sapiens

<400> 109

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
50 55 50

Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
65 70 75 80

Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
100 105 110

Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
165 170 175

Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
180 185 190

Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp

210

215

220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240

Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu  
 275 280 285

Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala  
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn  
 305 310 315 320

Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro  
 325 330 335

Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln  
 340 345 350

Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro  
 355 360 365

Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His  
 370 375 380

Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
 385 390 395 400

Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser  
 405 410 415

Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro  
 420 425 430

Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val  
 435 440 445

Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu  
 450 455 460

Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln  
 465 470 475 480

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln  
 485 490 495

Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn  
 500 505 510

Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu  
 515 520 525

Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu  
 530 535 540

Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala  
 545 550 555 560

Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser  
 565 570 575

Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp  
 580 585 590

Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp  
 595 600 605

Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys  
 610 615 620

Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn  
 625 630 635 640

Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser  
 645 650 655

Gly Ser Met Glu Ile Ile Glu Val Ser  
 660 665

<210> 110  
 <211> 625  
 <212> PRT  
 <213> Homo sapiens

<400> 110

Met	Ala	Gly	Asp	Arg	Leu	Pro	Arg	Lys	Val	Met	Asp	Ala	Lys	Lys	Leu
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Ala	Ser	Leu	Leu	Arg	Gly	Gly	Pro	Gly	Gly	Pro	Leu	Val	Ile	Asp	Ser
		20					25						30		
Arg	Ser	Phe	Val	Glu	Tyr	Asn	Ser	Trp	His	Val	Leu	Ser	Ser	Val	Asn
		35					40					45			
Ile	Cys	Cys	Ser	Lys	Leu	Val	Lys	Arg	Arg	Leu	Gln	Gln	Gly	Lys	Val
	50					55					60				
Thr	Ile	Ala	Glu	Leu	Ile	Gln	Pro	Ala	Ala	Arg	Ser	Gln	Val	Glu	Ala
65					70					75					80
Thr	Glu	Pro	Gln	Asp	Val	Val	Val	Tyr	Asp	Gln	Ser	Thr	Arg	Asp	Ala
				85					90					95	
Ser	Val	Leu	Ala	Ala	Asp	Ser	Phe	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Leu
			100					105					110		
Asp	Gly	Cys	Phe	Asp	Ser	Val	Ala	Ile	Leu	Thr	Gly	Gly	Phe	Ala	Thr
	115						120					125			
Phe	Ser	Ser	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Pro	Ala	Ala	Leu
	130					135					140				
Leu	Pro	Met	Ser	Leu	Ser	Gln	Pro	Cys	Leu	Pro	Val	Pro	Ser	Val	Gly
145					150					155					160
Leu	Thr	Arg	Ile	Leu	Pro	His	Leu	Tyr	Leu	Gly	Ser	Gln	Lys	Asp	Val
			165						170					175	
Leu	Asn	Lys	Asp	Leu	Met	Thr	Gln	Asn	Gly	Ile	Ser	Tyr	Val	Leu	Asn
			180					185					190		
Ala	Ser	Asn	Ser	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Cys	Glu	Ser	Arg	Phe
		195					200					205			
Met	Arg	Val	Pro	Ile	Asn	Asp	Asn	Tyr	Cys	Glu	Lys	Leu	Leu	Pro	Trp
	210					215					220				
Leu	Asp	Lys	Ser	Ile	Glu	Phe	Ile	Asp	Lys	Ala	Lys	Leu	Ser	Ser	Cys
225					230					235					240
Gln	Val	Ile	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile
				245					250					255	
Ala	Ile	Ala	Tyr	Ile	Met	Lys	Thr	Met	Gly	Met	Ser	Ser	Asp	Asp	Ala

260					265					270					
Tyr	Arg	Phe	Val	Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn
	275					280						285			
Phe	Leu	Gly	Gln	Leu	Leu	Glu	Tyr	Glu	Arg	Thr	Leu	Lys	Leu	Leu	Ala
	290					295					300				
Ala	Leu	Gln	Gly	Asp	Pro	Gly	Thr	Pro	Ser	Gly	Thr	Pro	Glu	Pro	Pro
305					310					315					320
Pro	Ser	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Pro	Arg	Leu	Pro	Pro	Pro	Thr
			325					330						335	
Ser	Glu	Ser	Ala	Ala	Thr	Gly	Asn	Ala	Ala	Ala	Arg	Glu	Gly	Gly	Leu
			340					345					350		
Ser	Ala	Gly	Gly	Glu	Pro	Pro	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Ser
	355						360					365			
Ala	Leu	Gln	Gln	Gly	Leu	Arg	Gly	Leu	His	Leu	Ser	Ser	Asp	Arg	Leu
	370					375					380				
Gln	Asp	Thr	Asn	Arg	Leu	Lys	Arg	Ser	Phe	Ser	Leu	Asp	Ile	Lys	Ser
385					390					395					400
Ala	Tyr	Ala	Pro	Ser	Arg	Arg	Pro	Asp	Gly	Pro	Gly	Pro	Pro	Asp	Pro
			405						410					415	
Gly	Glu	Ala	Pro	Lys	Leu	Cys	Lys	Leu	Asp	Ser	Pro	Ser	Gly	Ala	Ala
		420						425					430		
Leu	Gly	Leu	Ser	Ser	Pro	Ser	Pro	Asp	Ser	Pro	Asp	Ala	Ala	Pro	Glu
	435						440					445			
Ala	Arg	Pro	Arg	Pro	Arg	Arg	Arg	Pro	Arg	Pro	Pro	Ala	Gly	Ser	Pro
	450					455					460				
Ala	Arg	Ser	Pro	Ala	His	Ser	Leu	Gly	Leu	Asn	Phe	Gly	Asp	Ala	Ala
465					470					475					480
Arg	Gln	Thr	Pro	Arg	His	Gly	Leu	Ser	Ala	Leu	Ser	Ala	Pro	Gly	Leu
			485						490					495	
Pro	Gly	Pro	Gly	Gln	Pro	Ala	Gly	Pro	Gly	Ala	Trp	Ala	Pro	Pro	Leu
		500					505						510		
Asp	Ser	Pro	Gly	Thr	Pro	Ser	Pro	Asp	Gly	Pro	Trp	Cys	Phe	Ser	Pro
	515						520					525			
Glu	Gly	Ala	Gln	Gly	Ala	Gly	Gly	Val	Leu	Phe	Ala	Pro	Phe	Gly	Arg
	530					535					540				
Ala	Gly	Ala	Pro	Gly	Pro	Gly	Gly	Gly	Ser	Asp	Leu	Arg	Arg	Arg	Glu
545					550					555					560
Ala	Ala	Arg	Ala	Glu	Pro	Arg	Asp	Ala	Arg	Thr	Gly	Trp	Pro	Glu	Glu



Asp Ser Asp Gly Ser Pro Leu Ser Asn Ser Gln Pro Ser Phe Pro Val  
 195 200 205

Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala Lys Asp Ser Thr Asn  
 210 215 220

Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr Ile Leu Asn Val Thr  
 225 230 235 240

Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly Glu Phe Lys Tyr Lys  
 245 250 255

Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe  
 260 265 270

Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg Gly Lys Asn Cys Gly  
 275 280 285

Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr  
 290 295 300

Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser Met Asn Asp Ala Tyr  
 305 310 315 320

Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe  
 325 330 335

Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu Gly Leu Ser Ser Pro  
 340 345 350

Cys Asp Asn Arg Val Pro Ala Gln Gln Leu Tyr Phe Thr Thr Pro Ser  
 355 360 365

Asn Gln Asn Val Tyr Gln Val Asp Ser Leu Gln Ser Thr  
 370 375 380

<210> 112  
 <211> 482  
 <212> PRT  
 <213> Homo sapiens  
 <400> 112

Met Pro Pro Ser Pro Leu Asp Asp Arg Val Val Val Ala Leu Ser Arg  
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Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu  
 20 25 30

Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr  
 35 40 45

Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser  
 50 55 60

Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys  
 65 70 75 80

Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala  
 85 90 95  
 Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys  
 100 105 110  
 Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser  
 115 120 125  
 Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu  
 130 135 140  
 Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr  
 145 150 155 160  
 Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp  
 165 170 175  
 Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val  
 180 185 190  
 His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly  
 195 200 205  
 Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser  
 210 215 220  
 Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr  
 225 230 235 240  
 Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu  
 245 250 255  
 Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly  
 260 265 270  
 Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu  
 275 280 285  
 Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Ala Ala Ser  
 290 295 300  
 Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala  
 305 310 315 320  
 Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp  
 325 330 335  
 Ala Gln Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile  
 340 345 350  
 Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe  
 355 360 365  
 Asn Tyr Lys Arg Leu Pro Ala Thr Asp Ser Asn Lys Gln Asn Leu Arg  
 370 375 380



Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys  
 385 390 395 400  
 Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala  
 405 410 415  
 Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr  
 420 425 430  
 Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn  
 435 440 445  
 Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn  
 450 455 460  
 Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr  
 465 470 475 480  
 Val Val

<210> 113  
 <211> 2756  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (369)..(2348)

<400> 113  
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 atgaatctag tgtgaggggc tgctttgtgg aaggaatcct ttgcaagagc atatcaacag 180  
 gaaagagaaa gagacattca gttggagggc tcttgctgaa atggatttaa ctctcctctt 240  
 gccagtcacc actagcctga cctcatacat ttttagtaca atggagtggc tgagcctttg 300  
 agcacagcac cattacatca tcgtggcaaa ttaaagaacg aggtggggaa agaggactta 360  
 ttgttgtc atg gcc cat gag atg att gga act caa att gtt act gag agc 410  
 Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Ser  
 1 5 10  
 ttg gtg gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat 453  
 Leu Val Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp  
 15 20 25 30  
 agc cga cca ttt gtg gaa tac aat acg tct cac att ttg gaa gcc att 506  
 Ser Arg Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile  
 35 40 45  
 aat atc aac tgc tcc aaa ctg atg aag cga agg ttg caa cag gac aaa 554

Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys	
50 55 60	
gta tta att aga gaa cta atc cac caa tct aca aag cat aag gtt gac	692
Val Leu Ile Thr Glu Leu Ile His Gln Ser Thr Lys His Lys Val Asp	
65 70 75	
att gac tgc aat caa aga gtg gta gtt tat gat cac agt tca caa gat	650
Ile Asp Cys Asn Gln Arg Val Val Val Tyr Asp His Ser Ser Gln Asp	
80 85 90	
gtt ggt tct ctg tct tca gac tgc ttt ctc act gta ctt ctg ggt aag	693
Val Gly Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys	
95 100 105 110	
ctg gag aga agc ttc aac tct gtc cac ctg ctt gca ggt ggc ttt gct	746
Leu Glu Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala	
115 120 125	
gag ttc tct cgt tgt ttc cct ggc ctc tgt gaa gga aag tcc act cta	794
Glu Phe Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu	
130 135 140	
gtc cct acc tgc ata tct cag cct tgc tta cct gtt gcg aac att ggg	842
Val Pro Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly	
145 150 155	
cca act cga att ctt ccc aat ctc tat ctt ggc tgc cag cga gat gtc	890
Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val	
160 165 170	
ctc aac aag gac ctg atg caa cag aat ggg att ggc tat gtg tta aat	938
Leu Asn Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn	
175 180 185 190	
gcc agc aat acc tgt cca aag cct gac ttc ata cct gaa tct cac ttc	986
Ala Ser Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe	
195 200 205	
ctg cga gtg cct gtg aat gac agc ttt tgt gag aaa atc cta cca tgg	1034
Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp	
210 215 220	
ttg gac aag tct gtg gat ttc att gag aaa gca aaa gcc tcc aat ggc	1082
Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly	
225 230 235	
tgt gtg ctt atc cac tgc tta gct ggg atc tct cgc tcc gcc act att	1130
Cys Val Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile	
240 245 250	
gct att gcc tac atc atg aag agg atg gac atg tct cta gat gag gct	1178
Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala	
255 260 265 270	
tac aga ttt gtg aaa gaa aaa aga cct act ata tct ccg aat ttt aat	1226
Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn	

275										280					285					
ttt atg ggc cca ctc atg gac tat gag aag acg att aat aac cag act	1274																			
Phe Met Gly Gln Leu Met Asp Tyr Glu Lys Thr Ile Asn Asn Gln Thr																				
290 295 300																				
gga atg tca ggg cca aag agc aaa ctg aag ctg ctg cac cta gac aaa	1322																			
Gly Met Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Asp Lys																				
305 310 315																				
ccc agt gag ccc gtg cct gca gcc tca gag ggc gga tgg aag agt gca	1370																			
Pro Ser Glu Pro Val Pro Ala Ala Ser Glu Gly Gly Trp Lys Ser Ala																				
320 325 330																				
ctg tct ctc agt cca ccc tgt gcc aac tcg acc tcg gag gca tca ggg	1413																			
Leu Ser Leu Ser Pro Pro Cys Ala Asn Ser Thr Ser Glu Ala Ser Gly																				
335 340 345 350																				
caa agg ctt gtg cat cct gca agt gtg ccc cgc tta cag ccg tca ctc	1466																			
Gln Arg Leu Val His Pro Ala Ser Val Pro Arg Leu Gln Pro Ser Leu																				
355 360 365																				
tta gag gac agt ccc ctg gta cag gcg ctc agt ggg ctc cag ctg tcc	1514																			
Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu Gln Leu Ser																				
370 375 380																				
tca gag aag ctg gaa gac agc act aag ctc aag cgt tcc ttc tct ctc	1562																			
Ser Glu Lys Leu Glu Asp Ser Thr Lys Leu Lys Arg Ser Phe Ser Leu																				
385 390 395																				
gat atc aaa tct gtt tca tat tca gcc agt atg gcc gcg tcc cta cac	1610																			
Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu His																				
400 405 410																				
ggc ttc tcg tca gag gag gct tta gac tac tgc aaa cct tct gcc aca	1653																			
Gly Phe Ser Ser Glu Glu Ala Leu Asp Tyr Cys Lys Pro Ser Ala Thr																				
415 420 425 430																				
ctg gat ggg acc aac aag ctc tgc cag ttc tcc ccc gtt cag gag gta	1706																			
Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln Glu Val																				
435 440 445																				
tca gaa cag agt cca gag acc agc ccg gat aag gag gag gcc cac atc	1754																			
Ser Glu Gln Ser Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala His Ile																				
450 455 460																				
ccc aag cag ccc caa cct ccc agg cct tct gag agc cag gtc aca cgc	1802																			
Pro Lys Gln Pro Gln Pro Pro Arg Pro Ser Glu Ser Gln Val Thr Arg																				
465 470 475																				
ttg cac tca gtg aga acc ggc agt agt ggg tcc acc cag agg ccc ttc	1850																			
Leu His Ser Val Arg Thr Gly Ser Ser Gly Ser Thr Gln Arg Pro Phe																				
480 485 490																				
ttc tcg cca ctg cat cgg agc ggg agt gta gag gac aat tac cat acc	1898																			
Phe Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr His Thr																				
495 500 505 510																				

aac ttc ctt ttt ggc ctt tcc acc agc cag caa cac ctc acc aag tct Asn Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr Lys Ser 515 520 525	1946
gca ggg ctt ggc ctc aag ggc tgg cac tca gat att ctg gct ccc cag Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala Pro Gln 530 535 540	1994
tcc tct gcc ccc tcc ctg acc agc agt tgg tat ttt gct acg gag cct Ser Ser Ala Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr Glu Pro 545 550 555	2042
tca cac ttg tac tct gct tca gcc atc tat gga ggc aac agc agt tac Ser His Leu Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Asn Ser Ser Tyr 560 565 570	2090
tct gcc tac agc tgt ggc cag ctg ccc act tgc agt gac caa atc tat Ser Ala Tyr Ser Cys Gly Gln Leu Pro Thr Cys Ser Asp Gln Ile Tyr 575 580 585 590	2138
tct gtt cgt agg cgg cag aag cct act gac aga gct gac tcg agg cgg Ser Val Arg Arg Arg Gln Lys Pro Thr Asp Arg Ala Asp Ser Arg Arg 595 600 605	2186
agc tgg cat gaa gag agc ccc ttt gaa aag cag ttt aaa cgc aga agc Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg Arg Ser 610 615 620	2234
tgc caa atg gaa ttt gga gag agc att atg tgg gag aac agg tcc agg Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg 625 630 635	2282
gag gag ctg ggc aag gtg ggc agc cag tcc agc ttc tcc ggc agc atg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met 640 645 650	2330
gag atc atc gag gtc tct tgagaagacc tcgtcgttcc tgttgacagt Glu Ile Ile Glu Val Ser 655 660	2378
tttgtttcct gttcacaaaa aatagtcctt gtaaacttga aatatgtata tgtacataca	2438
tatatatttt tggaatatag agctacggtta taaaagcaac agatggatca acacagttgt	2498
tctctcagca cctgcactga gaatagctaa ctctcagaaa agattggaag ggtagatggt	2558
agaattctcc cagccaggag aagagatttg gttcagtga ttgcacatct tcttgttcct	2618
acaaaagcaa gggttttgtt tgtttgatg ttgtttgttt ttaatgtag agggcaaaat	2678
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agtgcacctt agcgctaa	2756

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<211> 660  
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 <213> Mus musculus

<400> 114

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 20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
 35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
 50 55 60

Ile Thr Glu Leu Ile His Gln Ser Thr Lys His Lys Val Asp Ile Asp  
 65 70 75 80

Cys Asn Gln Arg Val Val Val Tyr Asp His Ser Ser Gln Asp Val Gly  
 85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
 100 105 110

Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
 115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
 130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
 145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
 165 170 175

Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
 180 185 190

Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
 195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
 210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240

Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Met  
 275 280 285

Gly Gln Leu Met Asp Tyr Glu Lys Thr Ile Asn Asn Gln Thr Gly Met  
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Asp Lys Pro Ser  
 305 310 315 320

Glu Pro Val Pro Ala Ala Ser Glu Gly Gly Trp Lys Ser Ala Leu Ser  
 325 330 335

Leu Ser Pro Pro Cys Ala Asn Ser Thr Ser Glu Ala Ser Gly Gln Arg  
 340 345 350

Leu Val His Pro Ala Ser Val Pro Arg Leu Gln Pro Ser Leu Leu Glu  
 355 360 365

Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu Gln Leu Ser Ser Glu  
 370 375 380

Lys Leu Glu Asp Ser Thr Lys Leu Lys Arg Ser Phe Ser Leu Asp Ile  
 385 390 395 400

Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu His Gly Phe  
 405 410 415

Ser Ser Glu Glu Ala Leu Asp Tyr Cys Lys Pro Ser Ala Thr Leu Asp  
 420 425 430

Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln Glu Val Ser Glu  
 435 440 445

Gln Ser Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala His Ile Pro Lys  
 450 455 460

Gln Pro Gln Pro Pro Arg Pro Ser Glu Ser Gln Val Thr Arg Leu His  
 465 470 475 480

Ser Val Arg Thr Gly Ser Ser Gly Ser Thr Gln Arg Pro Phe Phe Ser  
 485 490 495

Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr His Thr Asn Phe  
 500 505 510

Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr Lys Ser Ala Gly  
 515 520 525

Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala Pro Gln Ser Ser  
 530 535 540

Ala Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr Glu Pro Ser His  
 545 550 555 560

Leu Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Asn Ser Ser Tyr Ser Ala  
 565 570 575

Tyr Ser Cys Gly Gln Leu Pro Thr Cys Ser Asp Gln Ile Tyr Ser Val  
 580 585 590

Arg Arg Arg Gln Lys Pro Thr Asp Arg Ala Asp Ser Arg Arg Ser Trp  
 595 600 605

His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg Arg Ser Cys Gln  
 610 615 620

Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu  
 625 630 635 640

Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met Glu Ile  
 645 650 655

Ile Glu Val Ser

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 <212> DNA  
 <213> Homo sapiens

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 agggaggtggg aaaagaggac ttattgttgt catggcccat gagatgattg gaactcaaat 120  
 tgttactgag aggttggtgg ctctgctgga aagtggaaacg gaaaaagtgc tgctaattga 180  
 tagccggcca tttgtggaat acaatacatc ccacattttg gaagccatta atatcaactg 240  
 ctccaagcct atgaagcgaa ggttgcaaca ggacaaagtg ttaattacag agctcatcca 300  
 gcattcagcg aaacataagg ttgacattga ttgcagtcag aaggttgtag ttacgatca 360  
 aagctcccaa gatgttgccct ctctctcttc agactgtttt ctcaactgt 408

<210> 116  
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 <212> PRT  
 <213> Homo sapiens

<400> 116  
 Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu  
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<210> 117  
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 <213> Homo sapiens

<400> 117  
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 1 5 10

<210> 118  
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 Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile  
 1 5 10

<210> 119  
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<213> Homo sapiens

<400> 119

Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp  
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<210> 120

<211> 13

<212> PFT

<213> Homo sapiens

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Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
1 5 10

<210> 121

<211> 13

<212> PFT

<213> Homo sapiens

<400> 121

Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser  
1 5 10

<210> 122

<211> 13

<212> PFT

<213> Homo sapiens

<400> 122

Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln  
1 5 10

<210> 123

<211> 13

<212> PFT

<213> Homo sapiens

<400> 123

Pro Ser Asp Ser Gln Ser Lys Arg Leu His Ser Val Arg  
1 5 10

<210> 124

<211> 13

<212> PFT

<213> Homo sapiens

<400> 124

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly  
1 5 10

<210> 125  
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<212> PFT  
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<400> 125

Gly Asp Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro  
1 5 10

<210> 126  
<211> 13  
<212> PFT  
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<400> 126

Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser Arg Arg  
1 5 10

<210> 127  
<211> 13  
<212> PFT  
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<400> 127

Ser Asp Arg Ala Asp Ser Arg Arg Ser Trp His Glu Glu  
1 5 10

<210> 128  
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<212> PFT  
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<400> 128

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile  
1 5 10

<210> 129  
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<212> PFT  
<213> Homo sapiens

<400> 129

Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg  
1 5 10

<210> 130  
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<400> 130

Ile Gly Tyr Val Leu Asn Ala Ser Tyr Thr Cys Pro Lys Pro  
 1 5 10

<210> 131  
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 <212> PRT  
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<400> 131

Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu  
 1 5 10

<210> 132  
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 <212> PRT  
 <213> Homo sapiens

<400> 132

Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys  
 1 5 10

<210> 133  
 <211> 14  
 <212> PRT  
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<400> 133

Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys  
 1 5 10

<210> 134  
 <211> 140  
 <212> PRT  
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<400> 134

Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp  
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Val Leu Asn Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu  
 20 25 30

Asn Ala Ser Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His  
 35 40 45

Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro  
 50 55 60

Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn  
 65 70 75 80

Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr  
 85 90 95

Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu  
100 105 110

Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe  
115 120 125

Asn Phe Leu Gly Gln Leu Leu Asp Tyr Glu Lys Lys  
130 135 140

<210> 135  
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<213> Mus musculus

<400> 135

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Val Leu Asn Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu  
20 25 30

Asn Ala Ser Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His  
35 40 45

Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro  
50 55 60

Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn  
65 70 75 80

Gly Cys Val Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr  
85 90 95

Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu  
100 105 110

Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe  
115 120 125

Asn Phe Met Gly Gln Leu Met Asp Tyr Glu Lys Thr  
130 135 140

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38

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<400> 137  
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<210> 138  
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<400> 138  
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<210> 143  
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 gcagcagtcg accgtcttct catagtccat gagttgg 37

<210> 144  
 <211> 2'  
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<400> 144

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 1 5 10 15

Thr Ile Ala Ile Ala Tyr Ile  
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<210> 146  
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 <212> DNA  
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<400> 146  
 tgetgctctg ctaccaaccc 30

<210> 147  
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 <212> DNA  
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<400> 147  
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 gtgacaactt tcgtttccct ctgagggaat tgggaggtcg gcggcccca aagctttcag 180  
 tccagtgtaa agctgttgga gcgcgggagc aaaggtaaag aatgatgtaa tgcgtggct 240  
 gctccaaaagc atcttttgtt gtggaatggt tattccagtc atctctttat gaatcaaatg 300  
 tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga 360  
 gacattcact tggagggctc ttgctgaaaa tgggtttaac tctcttttg ccagtcacca 420

ccagcctgac ctcataaact tttagtacaa tggagtgggt gagcctttga gcacaccacc 480

attacatcat cgtggcgaat taaagaagga ggtgggaaaa gaggacttat tgttgtc 537

atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg 585  
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg 633  
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
20 25 30

cca ttt gtg gaa tac aat aca tcc cac att ttg gaa gcc att aat atc 681  
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
35 40 45

aac tgc tcc aag ctt atg aag cga agg ttg caa cag gac aaa gtg tta 729  
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
50 55 60

att aca gag ctc atc cag cat tca gcg aaa cat aag gtt gac att gat 777  
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
65 70 75 80

tgc agt cag aag gtt gta gtt tac gat caa agc tcc caa gat gtt gcc 825  
Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
85 90 95

tct ctc tct tca gac tgt ttt ctc act gta ctt ctg ggt aaa ctg gag 873  
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
100 105 110

aag agc ttc aac tct gtt cac ctg ctt gca ggt ggg ttt gct gag ttc 921  
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
115 120 125

tct cgt tgt ttc cct ggc ctc tgt gaa gga aaa tcc act cta gtc cct 969  
Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
130 135 140

acc tgc att tct cag cct tgc tta cct gtt gcc aac att ggg cca acc 1017  
Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
145 150 155 160

cga att ctt ccc aat ctt tat ctt ggc tgc cag cga gat gtc ctc aac 1065  
Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
165 170 175

aag gag ctg ata cag cag aat ggg att ggt tat gtg tta aat gcc agc 1113  
Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
180 185 190

tat acc tgt cca aag cct gac ttt atc ccc gag tct cat ttc ctg cgt 1161  
Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
195 200 205

gtg cct gtg aat gac agc ttt tgt gag aaa att ttg cag tgg ttg gac 1209

Val	Pro	Val	Asn	Asp	Ser	Phe	Cys	Glu	Lys	Ile	Leu	Pro	Trp	Leu	Asp		
210						215					220						
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Lys	Ser	Val	Asp	Phe	Ile	Glu	Lys	Ala	Lys	Ala	Ser	Asn	Gly	Cys	Val		
225					230					235					240		
cta	gtg	cac	tgt	tta	gct	ggg	atc	tcc	cgc	tcc	gac	acc	atc	gct	atc	1305	
Leu	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	Ala	Ile		
				245				250						255			
gcc	tac	atc	atg	aag	agg	atg	gac	atg	tct	tta	gat	gaa	gct	tac	aga	1353	
Ala	Tyr	Ile	Met	Lys	Arg	Met	Asp	Met	Ser	Leu	Asp	Glu	Ala	Tyr	Arg		
			260					265					270				
ttt	gtg	aaa	gaa	aaa	aga	cct	act	ata	tct	cca	aac	ttc	aat	ttt	ctg	1401	
Phe	Val	Lys	Glu	Lys	Arg	Pro	Thr	Ile	Ser	Pro	Asn	Phe	Asn	Phe	Leu		
		275					280					285					
ggc	caa	ctc	ctg	gac	tat	gag	aag	aag	att	aag	aac	cag	act	gga	gca	1449	
Gly	Gln	Leu	Leu	Asp	Tyr	Glu	Lys	Lys	Ile	Lys	Asn	Gln	Thr	Gly	Ala		
		290					295				300						
tca	ggg	cca	aag	agc	aaa	ctc	aag	ctg	ctg	cac	ctg	gag	aag	cca	aat	1497	
Ser	Gly	Pro	Lys	Ser	Lys	Leu	Lys	Leu	Leu	His	Leu	Glu	Lys	Pro	Asn		
305					310					315					320		
gaa	cct	gtc	cct	gct	gtc	tca	gag	ggg	gga	cag	aaa	agc	gag	acg	ccc	1545	
Glu	Pro	Val	Pro	Ala	Val	Ser	Glu	Gly	Gly	Gln	Lys	Ser	Glu	Thr	Pro		
				325					330					335			
ctc	agt	cca	ccc	tgt	gcc	gac	tct	gct	acc	tca	gag	gca	gca	gga	caa	1593	
Leu	Ser	Pro	Pro	Cys	Ala	Asp	Ser	Ala	Thr	Ser	Glu	Ala	Ala	Gly	Gln		
			340					345					350				
agg	ccc	gtg	cat	ccc	gcc	agc	gtg	ccc	agc	gtg	ccc	agc	gtg	cag	ccg	1641	
Arg	Pro	Val	His	Pro	Ala	Ser	Val	Pro	Ser	Val	Pro	Ser	Val	Gln	Pro		
		355					360					365					
tcg	ctg	tta	gag	gac	agc	ccg	ctg	gta	cag	gcg	ctc	agt	ggg	ctg	cac	1689	
Ser	Leu	Leu	Glu	Asp	Ser	Pro	Leu	Val	Gln	Ala	Leu	Ser	Gly	Leu	His		
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Leu	Ser	Ala	Asp	Arg	Leu	Glu	Asp	Ser	Asn	Lys	Leu	Lys	Arg	Ser	Phe		
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Ser	Leu	Asp	Ile	Lys	Ser	Val	Ser	Tyr	Ser	Ala	Ser	Met	Ala	Ala	Ser		
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tta	cat	ggc	ttc	tcc	tca	tca	gaa	gat	gct	ttg	gaa	tac	tac	aaa	cct	1833	
Leu	His	Gly	Phe	Ser	Ser	Ser	Glu	Asp	Ala	Leu	Glu	Tyr	Tyr	Lys	Pro		
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tcc	act	act	ctg	gat	ggg	acc	aac	aag	cta	tgc	cag	ttc	tcc	cct	gtt	1881	
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Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu			
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Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln			
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Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp			
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Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
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490

495

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tgaaatgcca aatgctaaat gcagtgttct ttcacactgt ttttaatttc ttgggaatt	3978
gagtccagtg gatgttaatg gagtgggttg ccacacctg aaatgtctta ttttcaagtg	4038

cctggcctgg gaaagaaggg gaagaaacaa ttgcattata tccaaagata cactataaaa 4098  
 atagagtttt taccaaaaaa agatgtttgt tctcatctca gtaggcctca tttgggcaag 4158  
 tgacccacag gtcttttggc gagtttgcta tttgcctgtt gaaatacttg tttcaactta 4218  
 gagaacagtt atgatgtgac catagcatgg cacaactaaa aatctaagcc tgaaacctga 4278  
 aaaaagagat atgacaaggg aaattaatca ggctatacat aagtattgta tttatttgaa 4338  
 taaaaataaa aagagcaacc cataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaag 4393

<210> 150  
 <211> 607  
 <212> PFT  
 <213> Homo sapiens

<400> 150

Met Glu Ala Gly Ile Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly  
 1 5 10 15

Val Ala Ser Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe  
 20 25 30

Ala Leu Gln Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly  
 35 40 45

Arg Thr Gly Val Leu Ile Ala Cys Tyr Leu Val Phe Ala Thr Arg Met  
 50 55 60

Thr Ala Asp Gln Ala Ile Ile Phe Val Arg Ala Lys Arg Pro Asn Ser  
 65 70 75 80

Ile Gln Thr Arg Gly Gln Leu Leu Cys Val Arg Glu Phe Thr Gln Phe  
 85 90 95

Leu Thr Pro Leu Arg Asn Ile Phe Ser Cys Cys Asp Pro Lys Ala His  
 100 105 110

Ala Val Thr Leu Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His  
 115 120 125

Gly Tyr Glu Ala Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu  
 130 135 140

Val Cys Lys Leu Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met

145	150	155	160
Lys Asp Val Ser Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr	155	170	175
Met Ser Glu Met Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His	180	185	190
Asp Ser Asp Val Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp	195	200	205
Phe Asp Asn Arg Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro	210	215	220
Leu Trp Lys Arg Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu	225	230	235
Lys Arg Arg Leu Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn	245	250	255
Leu Leu Glu Gln Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu	260	265	270
Val Gly His Lys Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile	275	280	285
Pro Gln Ser Pro Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser	290	295	300
Thr Leu Ser Phe Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu	305	310	315
Lys Asp Asn Gly Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu	325	330	335
Ala Gln Gln Ser Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser	340	345	350
Pro Gly Glu Pro Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro	355	360	365
Asn Pro Ala His Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly	370	375	380

Val Gly Ser Pro Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser  
 385 390 395 400

Pro Leu Asp Cys Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His  
 405 410 415

Glu Thr Gln Asp Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala  
 420 425 430

Leu Gln Ser Glu Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys  
 435 440 445

Ala Leu Ala Asn Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg  
 450 455 460

Lys Val Glu Met Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp  
 465 470 475 480

Glu Arg Ile Cys Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met  
 485 490 495

Trp Ser Trp Val Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp  
 500 505 510

Val Asp Met Leu Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe  
 515 520 525

Leu Leu Glu Lys Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys  
 530 535 540

Ile Val Asn Leu Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu  
 545 550 555 560

Ala His Ala Ile Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn  
 565 570 575

Gly Pro Thr Val Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu  
 580 585 590

Glu Glu Lys Arg Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu  
 595 600 605

<210> 151  
 <211> 378  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 151
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acccgctgtc ctgtgccctt tcccagcg atg ggc gtg cag ccc ccc aac ttc      112
                Met Gly Val Gln Pro Pro Asn Phe
                1                5

tcc tgg gtg ctt ccg ggc cgg ctg gcg gga ctg gcg ctg ccg cgg ctc      160
Ser Trp Val Leu Pro Gly Arg Leu Ala Gly Leu Ala Leu Pro Arg Leu
    10                15                20

ccc gcc cac tac cag ttc ctg ttg gac ctg ggc gtg cgg cac ctg gtg      208
Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg His Leu Val
    25                30                35                40

tcc ctg acg gag cgc ggg ccc cct cac agc gac agc tgc ccc ggc ctc      256
Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys Pro Gly Leu
                45                50                55

acc ctg cac cgc ctg cgc atc ccc gac ttc tgc ccg ccg gcc ccc gac      304
Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro Ala Pro Asp
                60                65                70

cag atc gac cgc ttc gtg cag atc gtg gac gag gcc aac gca cgg gga      352
Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn Ala Arg Gly
    75                80                85

gag gct gtg gga gtg cac tgt gct ctg ggc ttt ggc cgc act ggc acc      400
Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg Thr Gly Thr
    90                95                100

atg ctg gcc tgt tac ctg gtg aag gag cgg ggc ttg gct gca gga gat      448
Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala Ala Gly Asp
    105                110                115                120

gcc att gct gaa atc cga cga cta cga ccc ggc tcc atc gag acc tat      496
Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Ser Ile Glu Thr Tyr
                125                130                135

gag cag gag aaa gca gtc ttc cag ttc tac cag cga acg aaa      538
Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr Lys
                140                145                150

taaggggct tagtaccctt ctaccaggcc ctcactcccc tcccccatgt tgtcgatggg      598

gcacagagatg aagggaagtg gactaaagta ttaaaccctc tagctcccat tggctgaaga      658

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cactgaagta gccacccct gcaggcaggt cctgattgaa ggggaggctt gtactgcttt 718  
 gttgaataaa tgagttttac gaaccaggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 778  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 838  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc 878

<210> 152  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 152

Met Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu  
 1 5 10 15

Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu  
 20 25 30

Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro  
 35 40 45

His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro  
 50 55 60

Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile  
 65 70 75 80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala  
 85 90 95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys  
 100 105 110

Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu  
 115 120 125

Arg Pro Gly Ser Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln  
 130 135 140

Phe Tyr Gln Arg Thr Lys  
 145 150

<210> 153

<211> 470  
 <212> PRT  
 <213> Homo sapiens

<400> 153

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Met Glu Ala Gly Ile Tyr Phe Asn Phe Gly Trp Lys Asp Tyr Gly Val
1          5          10          15

Ala Ser Leu Thr Thr Ile Asp Met Val Lys Val Met Thr Phe Ala Leu
20          25          30

Gln Glu Gly Lys Val Ile His Cys His Ala Gly Leu Gly Arg Thr Gly
35          40          45

Val Leu Ile Ala Tyr Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln
50          55          60

Ala Ile Ile Val Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg Gly
65          70          75          80

Gln Leu Cys Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu Arg Asn
85          90          95

Ile Ser Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu Pro Gln Tyr
100         105         110

Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala Arg Leu Leu His
115         120         125

Val Pro Lys Ile Ile His Leu Val Cys Lys Leu Leu Leu Asp Ala Glu
130         135         140

Asn Arg Pro Val Met Met Lys Asp Val Ser Glu Gly Pro Leu Ser Ala
145         150         155         160

Glu Ile Glu Lys Thr Met Ser Glu Met Val Thr Met Leu Asp Lys Glu
165         170         175

Leu Leu Arg His Asp Ser Asp Val Ser Asn Pro Asn Pro Thr Ala Val
180         185         190

Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Ser Asn Glu Gln Gln Phe
195         200         205

Asp Pro Leu Trp Lys Arg Arg Asn Val Cys Leu Gln Pro Leu Thr His
210         215         220

Leu Lys Arg Arg Leu Ser Tyr Ser Ser Asp Leu Lys Arg Ala Glu Asn
225         230         235         240

Leu Leu Glu Gln Gly Glu Thr Gln Thr Val Pro Ala Gln Ile Leu Val
245         250         255

Gly His Lys Pro Arg Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln
260         265         270

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Ser Pro Glu Pro Asp His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser  
 275 280 285  
 Phe Trp Ser Gln Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly  
 290 295 300  
 Ser Pro Ile His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly  
 305 310 315 320  
 Ala Phe Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser  
 325 330 335  
 Pro Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val  
 340 345 350  
 His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Gln  
 355 360 365  
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Lys Ala  
 370 375 380  
 Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Ser Glu Ala  
 385 390 395 400  
 Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Ala Arg Arg Ile  
 405 410 415  
 Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Val Glu Lys Glu Glu  
 420 425 430  
 Leu Lys Arg Lys Val Glu Met Trp Gln Lys Leu Asn Ser Arg Asp Gly  
 435 440 445  
 Ala Trp Glu Arg Ile Cys Gly Glu Arg Pro Phe Ile Leu Cys Ser Leu  
 450 455 460  
 Met Trp Ser Trp Val Glu  
 465 470

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 154  
 tacaatttcg gatggaagga ttat

24

<210> 155  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
 gcatgacaat ggatagctac ttt

23

<210> 156  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 155  
gagaaagcag tcttcacgtt ctac

24

<210> 157  
<211> 24  
<212> DNA  
<213> Homo sapiens

<400> 157  
atgggagcta gagggtttaa tact

24

<210> 158  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 153

Leu Thr Pro Leu Arg Asn Ile Ser Cys Cys Asp Pro Lys Ala  
1 5 10

<210> 159  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 159

Thr Leu Ser Phe Trp Ser Gln Lys Phe Gly Gly Leu Glu  
1 5 10

<210> 160  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 160

Val Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys  
1 5 10

<210> 161  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 161

Pro Leu Asp Cys Gly Ser Ser Lys Ala Gln Phe Leu Val  
1 5 10

<210> 162  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 162

Pro Thr Val Tyr Asn Thr Lys Lys Ile Phe Lys His Thr  
 1 5 10

<210> 163  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 163

Gln Glu Gly Lys Val Ile His Cys His Ala Gly Leu Gly Arg Thr Gly  
 1 5 10 15

Val Leu Ile Ala Tyr Leu Val  
 20

<210> 164  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 164

Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg  
 1 5 10

<210> 165  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 165

His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro His Ser  
 1 5 10

<210> 166  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<400> 166

Gly Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg Thr Gly  
 1 5 10 15

Thr Met Leu Ala Cys Tyr Leu  
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<210> 167  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 167  
gcagcagcgg ccgcaatttc ggatggaagg attatggtg

39

<210> 168  
<211> 33  
<212> DNA  
<213> Homo sapiens

<400> 168  
gcagcagtcg acgaggccag gcttagggcc atc

33

<210> 169  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 169  
gcagcagcgg ccgcatggag gctggcattt acttctac

38

<210> 170  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 170  
gcagcagtcg accacccaag accacatcaa gctgc

35

<210> 171  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 171  
gcagcagcgg ccgcctgttg gacctgggcg tgcggcacc

39

<210> 172  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 172  
gcagcagtcg actttcgttc gctggtagaa ctggaag

37

<210> 173  
<211> 38  
<212> DNA

<213> Homo sapiens

<400> 173  
gcagcagcgg ccgcatgggc gtgcagcccc ccaacttc

38

<210> 174  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 174  
gcagcagtcg accaccaggt aacaggccag catggtg

37

<210> 175  
<211> 806  
<212> PRT  
<213> Homo sapiens

<400> 175

Met	Gln	Val	Gln	Asp	Ala	Thr	Arg	Arg	Pro	Ser	Ala	Val	Arg	Phe	Leu
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Ser	Ser	Phe	Leu	Gln	Gly	Arg	Arg	His	Ser	Thr	Ser	Asp	Pro	Val	Leu
			20					25					30		
Arg	Leu	Gln	Gln	Ala	Arg	Arg	Gly	Ser	Gly	Leu	Gly	Ser	Gly	Ser	Ala
			35				40					45			
Thr	Lys	Leu	Leu	Ser	Ser	Ser	Ser	Leu	Gln	Val	Met	Val	Ala	Val	Ser
	50						55				60				
Ser	Val	Ser	His	Ala	Glu	Gly	Asn	Pro	Thr	Phe	Pro	Glu	Arg	Lys	Arg
65					70					75					80
Asn	Leu	Glu	Arg	Pro	Thr	Pro	Lys	Tyr	Thr	Lys	Val	Gly	Glu	Arg	Leu
				85					90					95	
Arg	His	Val	Ile	Pro	Gly	His	Met	Ala	Cys	Ser	Met	Ala	Cys	Gly	Gly
			100					105					110		
Arg	Ala	Cys	Lys	Tyr	Glu	Asn	Pro	Ala	Arg	Trp	Ser	Glu	Gln	Glu	Gln
			115				120					125			
Ala	Ile	Lys	Gly	Val	Tyr	Ser	Ser	Trp	Val	Thr	Asp	Asn	Ile	Leu	Ala
			130				135				140				
Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	Tyr	His	Ile	Ile	Asp
145					150					155					160
Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	Asn	Leu	Gln	Arg	Pro
				165					170					175	
Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	Gln	Glu	Ser	Gly	Phe
				180				185					190		

Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly Ile Tyr Phe Tyr Asn  
 195 200 205  
 Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu Thr Thr Ile Leu Asp  
 210 215 220  
 Met Val Lys Val Met Thr Phe Ala Leu Gln Glu Gly Lys Val Ala Ile  
 225 230 235 240  
 His Cys His Ala Gly Leu Gly Arg Thr Gly Val Leu Ile Ala Cys Tyr  
 245 250 255  
 Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln Ala Ile Ile Phe Val  
 260 265 270  
 Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg Gly Gln Leu Leu Cys  
 275 280 285  
 Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu Arg Asn Ile Phe Ser  
 290 295 300  
 Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu Pro Gln Tyr Leu Ile  
 305 310 315 320  
 Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala Arg Leu Leu Lys His  
 325 330 335  
 Val Pro Lys Ile Ile His Leu Val Cys Lys Leu Leu Leu Asp Leu Ala  
 340 345 350  
 Glu Asn Arg Pro Val Met Met Lys Asp Val Ser Glu Gly Pro Gly Leu  
 355 360 365  
 Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met Val Thr Met Gln Leu  
 370 375 380  
 Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val Ser Asn Pro Pro Asn  
 385 390 395 400  
 Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser  
 405 410 415  
 Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg Arg Asn Val Glu Cys  
 420 425 430  
 Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser  
 435 440 445  
 Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln Gly Glu Thr Pro Gln  
 450 455 460  
 Thr Val Pro Ala Gln Ile Leu Val Gly His Lys Pro Arg Gln Gln Lys  
 465 470 475 480  
 Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro Glu Pro Asp Leu His  
 485 490 495

Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe Trp Ser Gln Ser Lys  
 500 505 510  
 Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly Ser Pro Ile Phe His  
 515 520 525  
 Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly Ala Phe Ser Ala  
 530 535 540  
 Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser Pro Ser Phe  
 545 550 555 560  
 Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val Ser His  
 565 570 575  
 Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Arg Gln  
 580 585 590  
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Pro Lys  
 595 600 605  
 Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Leu Ser  
 610 615 620  
 Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Glu Ala  
 625 630 635 640  
 Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Ser Val  
 645 650 655  
 Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met Trp Gln Lys Glu Leu  
 660 665 670  
 Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys Gly Glu Arg Asp Pro  
 675 680 685  
 Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val Glu Gln Leu Lys Glu  
 690 695 700  
 Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu Val Asp Arg Arg Ala  
 705 710 715 720  
 Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys Gly Gln His Gln Thr  
 725 730 735  
 Ile Leu Cys Val Leu His Cys Ile Val Asn Leu Gln Thr Ile Pro Val  
 740 745 750  
 Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile Lys Ala Phe Thr Lys  
 755 760 765  
 Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Leu Lys  
 770 775 780  
 Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp  
 785 790 795 800

Gly Pro Lys Pro Gly Leu  
805

<210> 176  
<211> 747  
<212> PRT  
<213> Homo sapiens

<400> 176

Met	Val	Ala	Val	Ser	Ser	Val	Ser	His	Ala	Glu	Gly	Asn	Pro	Thr	Phe	1	5	10	15
Pro	Glu	Arg	Lys	Arg	Asn	Leu	Glu	Arg	Pro	Thr	Pro	Lys	Tyr	Thr	Lys	20	25	30	
Val	Gly	Glu	Arg	Leu	Arg	His	Val	Ile	Pro	Gly	His	Met	Ala	Cys	Ser	35	40	45	
Met	Ala	Cys	Gly	Gly	Arg	Ala	Cys	Lys	Tyr	Glu	Asn	Pro	Ala	Arg	Trp	50	55	60	
Ser	Glu	Gln	Glu	Gln	Ala	Ile	Lys	Gly	Val	Tyr	Ser	Ser	Trp	Val	Thr	65	70	75	80
Asp	Asn	Ile	Leu	Ala	Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	85	90	95	
Tyr	His	Ile	Ile	Asp	Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	100	105	110	
Asn	Leu	Gln	Arg	Pro	Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	115	120	125	
Gln	Glu	Ser	Gly	Phe	Thr	Tyr	Leu	Pro	Glu	Ala	Phe	Met	Glu	Ala	Gly	130	135	140	
Ile	Tyr	Phe	Tyr	Asn	Phe	Gly	Trp	Lys	Asp	Tyr	Gly	Val	Ala	Ser	Leu	145	150	155	160
Thr	Thr	Ile	Leu	Asp	Met	Val	Lys	Val	Met	Thr	Phe	Ala	Leu	Gln	Glu	165	170	175	
Gly	Lys	Val	Ala	Ile	His	Cys	His	Ala	Gly	Leu	Gly	Arg	Thr	Gly	Val	180	185	190	
Leu	Ile	Ala	Cys	Tyr	Leu	Val	Phe	Ala	Thr	Arg	Met	Thr	Ala	Asp	Gln	195	200	205	
Ala	Ile	Ile	Phe	Val	Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg	210	215	220	
Gly	Gln	Leu	Leu	Cys	Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu	225	230	235	240
Arg	Asn	Ile	Phe	Ser	Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu				



245	250	255
Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala 260 265 270		
Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu Val Cys Lys Leu 275 280 285		
Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met Lys Asp Val Ser 290 295 300		
Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met 305 310 315 320		
Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val 325 330 335		
Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg 340 345 350		
Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg 355 360 365		
Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu 370 375 380		
Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln 385 390 395 400		
Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu Val Gly His Lys 405 410 415		
Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro 420 425 430		
Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe 435 440 445		
Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly 450 455 460		
Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser 465 470 475 480		
Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro 485 490 495		
Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His 500 505 510		
Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro 515 520 525		
Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys 530 535 540		
Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp		



Asn Leu Gln Arg Pro Gly Glu His Ala Ser Cys Gly Asn Pro Leu Glu  
 65 70 75 80  
 Gln Glu Ser Gly Phe Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly  
 85 90 95  
 Ile Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu  
 100 105 110  
 Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln Glu  
 115 120 125  
 Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly Val  
 130 135 140  
 Leu Ile Ala Cys Tyr Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln  
 145 150 155 160  
 Ala Ile Ile Phe Val Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg  
 165 170 175  
 Gly Gln Leu Leu Cys Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu  
 180 185 190  
 Arg Asn Ile Phe Ser Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu  
 195 200 205  
 Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala  
 210 215 220  
 Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu Val Cys Lys Leu  
 225 230 235 240  
 Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met Lys Asp Val Ser  
 245 250 255  
 Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met  
 260 265 270  
 Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val  
 275 280 285  
 Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg  
 290 295 300  
 Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg  
 305 310 315 320  
 Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu  
 325 330 335  
 Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln  
 340 345 350  
 Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu Val Gly His Lys  
 355 360 365

Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro  
 370 375 380

Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe  
 385 390 395 400

Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly  
 405 410 415

Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser  
 420 425 430

Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro  
 435 440 445

Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His  
 450 455 460

Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro  
 465 470 475 480

Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys  
 485 490 495

Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp  
 500 505 510

Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu  
 515 520 525

Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn  
 530 535 540

Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met  
 545 550 555 560

Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys  
 565 570 575

Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val  
 580 585 590

Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu  
 595 600 605

Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys  
 610 615 620

Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys Ile Val Asn Leu  
 625 630 635 640

Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile  
 645 650 655

Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val  
 660 665 670

Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg  
675 680 685

Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu  
690 695

<010> 178  
<011> 662  
<012> PRT  
<013> Homo sapiens

<400> 178

Met Ala Arg Pro Ser Ser Glu Leu Leu Glu Lys Tyr His Ile Ile Asp  
1 5 10 15

Gln Phe Leu Ser His Gly Ile Lys Thr Ile Ile Asn Leu Gln Arg Pro  
20 25 30

Gly Glu His Ala Ser Cys Gly Asn Pro Leu Glu Gln Glu Ser Gly Phe  
35 40 45

Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly Ile Tyr Phe Tyr Asn  
50 55 60

Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu Thr Thr Ile Leu Asp  
65 70 75 80

Met Val Lys Val Met Thr Phe Ala Leu Gln Glu Gly Lys Val Ala Ile  
85 90 95

His Cys His Ala Gly Leu Gly Arg Thr Gly Val Leu Ile Ala Cys Tyr  
100 105 110

Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln Ala Ile Ile Phe Val  
115 120 125

Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg Gly Gln Leu Leu Cys  
130 135 140

Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu Arg Asn Ile Phe Ser  
145 150 155 160

Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu Pro Gln Tyr Leu Ile  
165 170 175

Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala Arg Leu Leu Lys His  
180 185 190

Val Pro Lys Ile Ile His Leu Val Cys Lys Leu Leu Leu Asp Leu Ala  
195 200 205

Glu Asn Arg Pro Val Met Met Lys Asp Val Ser Glu Gly Pro Gly Leu  
210 215 220

Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met Val Thr Met Gln Leu  
225 230 235 240

Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val Ser Asn Pro Pro Asn  
 245 250 255  
 Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser  
 260 265 270  
 Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg Arg Asn Val Glu Cys  
 275 280 285  
 Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser  
 290 295 300  
 Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln Gly Glu Thr Pro Gln  
 305 310 315 320  
 Thr Val Pro Ala Gln Ile Leu Val Gly His Lys Pro Arg Gln Gln Lys  
 325 330 335  
 Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro Glu Pro Asp Leu His  
 340 345 350  
 Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe Trp Ser Gln Ser Lys  
 355 360 365  
 Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly Ser Pro Ile Phe His  
 370 375 380  
 Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly Ala Phe Ser Ala  
 385 390 395 400  
 Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser Pro Ser Phe  
 405 410 415  
 Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val Ser His  
 420 425 430  
 Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Arg Gln  
 435 440 445  
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Pro Lys  
 450 455 460  
 Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Leu Ser  
 465 470 475 480  
 Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Glu Ala  
 485 490 495  
 Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Ser Val  
 500 505 510  
 Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met Trp Gln Lys Glu Leu  
 515 520 525  
 Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys Gly Glu Arg Asp Pro  
 530 535 540

Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val Glu Gln Leu Lys Glu  
 545 550 555 560  
 Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu Val Asp Arg Arg Ala  
 565 570 575  
 Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys Gly Gln His Gln Thr  
 580 585 590  
 Ile Leu Cys Val Leu His Cys Ile Val Asn Leu Gln Thr Ile Pro Val  
 595 600 605  
 Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile Lys Ala Phe Thr Lys  
 610 615 620  
 Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Ile Lys  
 625 630 635 640  
 Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp  
 645 650 655  
 Gly Pro Lys Pro Gly Leu  
 660

<210> 179  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized Oligonucleotide.

<400> 179  
 ggauaucacu acugcauugc cugga

25

<210> 180  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized Oligonucleotide.

<400> 180  
 uatagcagau cugugcaggc caggu

25

<210> 181  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized Oligonucleotide.

<400> 181 25  
 ugacacaca guagcggaag augcu

<210> 182  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized Oligonucleotide.

<400> 182 25  
 agugaguagca gaaugguuag ccuuc

<210> 183  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized Oligonucleotide.

<400> 183 25  
 ugaaagcagg cgagauucga uccga

<210> 184  
 <211> 20  
 <212> DNA  
 <213> Homo sapiens

<400> 184 20  
 actaccgctt cacacgcttc

<210> 185  
 <211> 20  
 <212> DNA  
 <213> Homo sapiens

<400> 185 20  
 attgactaca gcagggcttc

<210> 186  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 186 26  
 atcaagtgtg acccagactg cctccg

<210> 187  
 <211> 28



<212> DNA  
 <213> Homo sapiens

<400> 187  
 ccatatgggat ccatggccca tgagattg

28

<210> 188  
 <211> 30  
 <212> DNA  
 <213> Homo sapiens

<400> 188  
 ggtaccctcg agtcaggaga cctcaatgat

30

<210> 189  
 <211> 30  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 ggtaccctcg agtcaagtct ggttcttaat

30

<210> 190  
 <211> 664  
 <212> PRT  
 <213> Homo sapiens

<400> 190

Met	Ala	His	Glu	Ile	Gly	Thr	Gln	Ile	Val	Thr	Glu	Arg	Leu	Val	Ala
1			5					10						15	
Leu	Leu	Glu	Ser	Gly	Thr	Glu	Lys	Val	Leu	Leu	Ile	Asp	Ser	Arg	Pro
		20					25						30		
Phe	Val	Glu	Tyr	Asn	Thr	Ser	His	Ile	Leu	Glu	Ala	Ile	Asn	Ile	Asn
	35					40						45			
Cys	Ser	Lys	Leu	Met	Lys	Arg	Arg	Leu	Gln	Gln	Asp	Lys	Val	Leu	Ile
	50				55						60				
Thr	Glu	Leu	Ile	Gln	His	Ser	Ala	Lys	His	Lys	Val	Asp	Ile	Asp	Cys
65				70					75					80	
Ser	Gln	Lys	Val	Val	Val	Tyr	Asp	Gln	Ser	Ser	Gln	Asp	Val	Ala	Ser
			85					90					95		
Leu	Ser	Ser	Asp	Cys	Phe	Leu	Thr	Val	Leu	Leu	Gly	Lys	Leu	Glu	Lys
			100					105					110		
Ser	Phe	Asn	Ser	Val	His	Leu	Leu	Ala	Gly	Gly	Phe	Ala	Glu	Phe	Ser
		115				120						125			
Arg	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Ser	Thr	Leu	Val	Pro	Thr

130	135	140
Cys Ile Ser Gln Pro	Cys Leu Pro Val Ala Asn Ile Gly Pro Thr Arg	
145	150	155 160
Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn Lys		
	165	170 175
Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser Asn		
	180	185 190
Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg Val		
	195	200 205
Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp Lys		
	210	215 220
Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val Leu		
225	230	235 240
Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile Ala		
	245	250 255
Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg Phe		
	260	265 270
Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu Gly		
	275	280 285
Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Ala Gly Ala Ser		
	290	295 300
Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn Glu		
305	310	315 320
Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro Leu		
	325	330 335
Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln Arg		
	340	345 350
Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro Ser		
	355	360 365
Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His Leu		
	370	375 380
Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe Ser		
385	390	395 400
Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu		
	405	410 415
His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro Ser		
	420	425 430
Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln		

435	440	445
Glu Leu Ser Glu Gln Thr	Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala	
450	455	460
Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln Ser		
465	470	475 480
Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln Arg		
485	490	495
Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr		
500	505	510
His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr		
515	520	525
Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala		
530	535	540
Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr		
545	550	555 560
Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser Ala		
565	570	575
Ser Tyr Ser Ala Tyr Ser Arg Ser Gln Leu Pro Thr Cys Gly Asp Gln		
580	585	590
Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser		
595	600	605
Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg		
610	615	620
Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg		
625	630	635 640
Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly		
645	650	655
Ser Met Glu Ile Ile Glu Val Ser		
660		

<210> 191  
 <211> 302  
 <212> PRT  
 <213> Homo sapiens

<400> 191

Met Ala His Glu Ile Val Gly Thr Gln Ile Val Thr Glu Arg Leu Val	
1 5 10 15	
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg	
20 25 30	

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
 35 40 45  
 Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
 50 55 60  
 Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
 65 70 75 80  
 Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
 85 90 95  
 Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
 100 105 110  
 Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
 115 120 125  
 Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
 130 135 140  
 Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
 145 150 155 160  
 Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
 165 170 175  
 Lys Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
 180 185 190  
 Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
 195 200 205  
 Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
 210 215 220  
 Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240  
 Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255  
 Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270  
 Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu  
 275 280 285  
 Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr  
 290 295 300

<110> 192  
 <111> 20  
 <112> PRT  
 <113> Artificial Sequence  
 <120>

<223> Synthesized Peptide.

<400> 193

Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys Ser Lys Lys Leu Lys Leu  
1 5 10 15

Leu His Leu Glu  
20

<210> 193

<211> 19

<212> PFT

<213> Artificial Sequence

<220>

<223> Synthesized Peptide.

<400> 193

Cys Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln Ser Lys Arg  
1 5 10 15

Leu His Ser

<210> 194

<211> 21

<212> DNA

<213> Homo sapiens

<400> 194

ctgcgtgttg cactgcatag t

21

<210> 195

<211> 19

<212> DNA

<213> Homo sapiens

<400> 195

tgggcaaggga aagcttcct

19

<210> 196

<211> 26

<212> DNA

<213> Homo sapiens

<400> 196

aacctgcaga caattcccgt ggatgt

26

<210> 197

<211> 21

<212> DNA

<213> Homo sapiens

<400> 197	21
gatatgccat tgetgaaatc c	
<210> 198	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 198	23
gactgcttcc tcttgetcat agg	
<210> 199	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 199	23
cgactacgac ccggtccat cga	
<210> 200	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 200	23
aggagcagat ggtagacgtg ttc	
<210> 201	
<211> 20	
<212> DNA	
<213> Homo sapiens	
<400> 201	20
ggctcagggt ctggatcatg	
<210> 202	
<211> 25	
<212> DNA	
<213> Homo sapiens	
<400> 202	25
tgctgtgcat gcactccgga tgcac	
<210> 203	
<211> 25	
<212> DNA	
<213> Homo sapiens	
<400> 203	25
cacataccaa atgtgtaaca gttca	

<210> 204  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 204  
 ggtactggtt tcctttctta aacatgt

27

<210> 205  
 <211> 35  
 <212> DNA  
 <213> Homo sapiens

<400> 205  
 cacttccaga gtgtgggtcat gccca

25

<210> 206  
 <211> 321  
 <212> PFT  
 <213> Homo sapiens

<400> 206

Met	Glu	Met	Glu	Lys	Glu	Phe	Glu	Gln	Ile	Asp	Lys	Ser	Gly	Ser	Trp	
1				5				10						15		
Ala	Ala	Ile	Tyr	Gln	Asp	Ile	Arg	His	Glu	Ala	Ser	Asp	Phe	Pro	Cys	
		20					25						30			
Arg	Val	Ala	Lys	Leu	Pro	Lys	Asn	Lys	Asn	Arg	Asn	Arg	Tyr	Arg	Asp	
		35					40					45				
Val	Ser	Pro	Phe	Asp	His	Ser	Arg	Ile	Lys	Leu	His	Gln	Glu	Asp	Asn	
	50					55					60					
Asp	Tyr	Ile	Asn	Ala	Ser	Leu	Ile	Lys	Met	Glu	Glu	Ala	Gln	Arg	Ser	
65				70					75					80		
Tyr	Ile	Leu	Thr	Gln	Gly	Pro	Leu	Pro	Asn	Thr	Cys	Gly	His	Phe	Trp	
			85					90						95		
Glu	Met	Val	Trp	Glu	Gln	Lys	Ser	Arg	Gly	Val	Val	Met	Leu	Asn	Arg	
		100						105					110			
Val	Met	Glu	Lys	Gly	Ser	Leu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Gln	Lys	
		115				120						125				
Glu	Glu	Lys	Glu	Met	Ile	Phe	Glu	Asp	Thr	Asn	Leu	Lys	Leu	Thr	Leu	
		130				135					140					
Ile	Ser	Glu	Asp	Ile	Lys	Ser	Tyr	Tyr	Thr	Val	Arg	Gln	Leu	Glu	Leu	
145				150					155					160		

Glu Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr  
 165 170 175

Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu  
 180 185 190

Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His  
 195 200 205

Gly Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr  
 210 215 220

Phe Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp  
 225 230 235 240

Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe  
 245 250 255

Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu  
 260 265 270

Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln  
 275 280 285

Asp Gln Trp Lys Glu Leu Ser His Glu Asp Leu Glu Pro Pro Pro Gly  
 290 295 300

His Ile Pro Pro Pro Pro Arg Pro Pro Lys Arg Ile Leu Glu Pro His  
 305 310 315 320

Asn

<210> 207  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 207

Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu Ser  
 1 5 10 15

Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu Val  
 20 25 30

Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile Pro  
 35 40 45

Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu Gly  
 50 55 60

Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp Ser  
 65 70 75 80

Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe Asn  
 85 90 95



Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala Leu  
 100 105 110

Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr Ser  
 115 120 125

Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys Met  
 130 135 140

Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile Gly  
 145 150 155 160

Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg Leu  
 165 170 175

Ala Lys Glu Gly Lys Leu Lys Pro  
 180

<210> 208

<211> 144

<212> PRT

<213> Homo sapiens

<400> 208

Ala Ser Phe Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala  
 1 5 10 15

Lys Asp Ser Thr Asn Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr  
 20 25 30

Ile Leu Asn Val Thr Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly  
 35 40 45

Glu Phe Lys Tyr Lys Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn  
 50 55 60

Leu Ser Gln Phe Phe Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg  
 65 70 75 80

Gly Lys Asn Cys Gly Val Leu Val His Ser Leu Ala Gly Ile Ser Arg  
 85 90 95

Ser Val Thr Val Thr Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser  
 100 105 110

Met Asn Asp Ala Tyr Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser  
 115 120 125

Pro Asn Phe Asn Phe Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu  
 130 135 140